

Gencore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2001, 23:56:33 ; Search time 1171.01 Seconds  
(without alignments)  
6989.746 Million cell updates/sec

Title: US-09-382-242-23  
Perfect score: 555  
Sequence: 1 ATGCTTTAAACAGCACTC.....AATCATACACTAACGATAG 555

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1283235 segs, 7373929652 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

- GenEmbl:\*  
1: gb\_ba1:\*  
2: gb\_ba2:\*  
3: gb\_ba3:\*  
4: gb\_in1:\*  
5: gb\_in2:\*  
6: gb\_in3:\*  
7: gb\_om:\*  
8: gb\_ov:\*  
9: gb\_pat1:\*  
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11: gb\_ph:\*  
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13: gb\_p12:\*  
14: gb\_p13:\*  
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17: em\_ba2:\*  
18: em\_fun:\*  
19: em\_htgo\_hum:\*  
20: em\_htgo\_inv:\*  
21: em\_htgo\_rod:\*  
22: em\_htg\_hum1:\*  
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28: em\_htg\_hum7:\*  
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30: em\_htg\_inv1:\*  
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C	13	20	3.6	155261	62	AC011921	Homo sapi	C	86	18	3.2	3140	59	HSEUNGS	L33971	Cottontail
C	14	20	3.6	159999	79	AL161417	Homo sapi	C	87	18	3.2	3211	88	AK000288	AK000288	Homo sapi
C	15	20	3.6	164746	69	AC025515	Homo sapi	C	88	18	3.2	3643	2	AF270154	AF270154	Staphyloc
C	16	20	3.6	174815	82	AP001390	Homo sapi	C	89	18	3.2	4571	85	AB051531	AB051531	Homo sapi
C	17	20	3.6	183836	79	AL163544	Homo sapi	C	90	18	3.2	7736	3	STH242480	STH242480	Streptococ
C	18	20	3.6	202553	61	AC009774	Homo sapi	C	91	18	3.2	12900	4	AE001429	AE001429	Plasmid
C	19	19	3.4	385	2	CPDHAT	X86487	C	92	18	3.2	22000	14	SPC229	SPC229	S. pombe
C	20	19	3.4	430	5	AF202766	Artemia p	C	93	18	3.2	24128	77	AC084416	AC084416	Artemia
C	21	19	3.4	430	5	AF202767	Artemia p	C	94	18	3.2	34617	12	AC004625	AC004625	Artemia
C	22	19	3.4	430	5	AF202768	Artemia p	C	95	18	3.2	39101	14	SPAC5747	SPAC5747	S. pombe
C	23	19	3.4	430	5	AF202769	Artemia p	C	96	18	3.2	42022	15	YSC19449	YSC19449	Saccharomy
C	24	19	3.4	430	5	AF202770	Artemia p	C	97	18	3.2	44410	4	AC084268	AC084268	Caenorhab
C	25	19	3.4	2213	94	AF035207	Mus muscu	C	98	18	3.2	54676	66	AC020213	AC020213	Drosophila
C	26	19	3.4	2940	94	AF153350	Mus muscu	C	99	18	3.2	57327	94	AC030318	AC030318	Mus muscu
C	27	19	3.4	9085	85	AB009808	Homo sapi	C	100	18	3.2	58943	70	AC025850	AC025850	Mus muscu
C	28	19	3.4	14230	93	HUMKEM1A	M86360	C	101	18	3.2	60153	69	AC025498	AC025498	Homo sapi
C	29	19	3.4	14537	93	HUMKEM1A	M86360	C	102	18	3.2	64650	74	AC068864	AC068864	Homo sapi
C	30	19	3.4	16388	3	U32830	M98447	C	103	18	3.2	71806	78	AC087464	AC087464	Homo sapi
C	31	19	3.4	50334	92	HS995012	U32830	C	104	18	3.2	74690	67	AC022581	AC022581	Homo sapi
C	32	19	3.4	71532	68	AC023655	AL035462	C	105	18	3.2	80689	4	AC003053	AC003053	Drosophila
C	33	19	3.4	92004	76	AC074230	AL035462	C	106	18	3.2	81293	12	AB018109	AB018109	Arabidops
C	34	19	3.4	93418	81	AL390955	AL390955	C	107	18	3.2	89004	6	CEY6982	CEY6982	Caenorhabd
C	35	19	3.4	114956	85	AC002072	AC002072	C	108	18	3.2	89934	12	AC007067	AC007067	Genomic s
C	36	19	3.4	116448	12	AC005142	AC005142	C	109	18	3.2	91916	12	AC005964	AC005964	Arabidops
C	37	19	3.4	139399	13	AP002865	AP002865	C	110	18	3.2	92918	66	AC020050	AC020050	Drosophila
C	38	19	3.4	140210	60	AC002993	AP002993	C	111	18	3.2	97348	94	AF091216	AF091216	Mus muscu
C	39	19	3.4	145174	88	AF289077	AF289077	C	112	18	3.2	98070	88	AC025463	AC025463	Homo sapi
C	40	19	3.4	147310	82	AL513495	AL117344	C	113	18	3.2	98119	83	HS015446	HS015446	Homo sapi
C	41	19	3.4	150336	92	HS7395C13	AL117344	C	114	18	3.2	98491	94	AF132039	AF132039	Mus muscu
C	42	19	3.4	155876	79	AL354809	AL354809	C	115	18	3.2	100605	78	AC087157	AC087157	Mus muscu
C	43	19	3.4	156780	77	AC083838	AC083838	C	116	18	3.2	102049	83	CEY51A2_3	CEY51A2_3	Caenorhabd
C	44	19	3.4	157090	85	AB019441	AB019441	C	117	18	3.2	106636	76	AC079437	AC079437	Homo sapi
C	45	19	3.4	159029	71	AC027201	AC027201	C	118	18	3.2	107484	91	HS424116	HS424116	Human DNA
C	46	19	3.4	159629	13	ATCHRIV9	AL161497	C	119	18	3.2	108581	69	AC025458	AC025458	Homo sapi
C	47	19	3.4	159716	70	AC025807	AC025807	C	120	18	3.2	109508	66	AC020813	AC020813	Mus muscu
C	48	19	3.4	163797	70	AC025872	AC025872	C	121	18	3.2	110312	94	AF131866	AF131866	Mus muscu
C	49	19	3.4	166758	85	AC003046	AC003046	C	122	18	3.2	110000	75	AC073702_1	AC073702_1	Continuation (2 of
C	50	19	3.4	167172	87	AC009428	AC009428	C	123	18	3.2	110000	75	AC073804_0	AC073804_0	Continuation (2 of
C	51	19	3.4	167977	81	AL451129	AL451129	C	124	18	3.2	110000	75	AC073804_1	AC073804_1	Continuation (2 of
C	52	19	3.4	169383	69	AP001598	AP001598	C	125	18	3.2	110000	75	AC073804_2	AC073804_2	Continuation (3 of
C	53	19	3.4	171038	90	AP001598	AP001598	C	126	18	3.2	110000	75	AC073804_2	AC073804_2	Continuation (3 of
C	54	19	3.4	171267	72	AC040979	AC040979	C	127	18	3.2	110000	77	AC083893_1	AC083893_1	Continuation (3 of
C	55	19	3.4	171502	72	AC046152	AC046152	C	128	18	3.2	110312	94	AF131866	AF131866	Mus muscu
C	56	19	3.4	172596	61	AC009707	AC009707	C	129	18	3.2	110680	12	AC006259	AC006259	Arabidops
C	57	19	3.4	174768	76	AC079191	AC079191	C	130	18	3.2	111775	94	AC018559	AC018559	Mus muscu
C	58	19	3.4	174798	79	AL157889	AL157889	C	131	18	3.2	113249	74	AC068805	AC068805	Mus muscu
C	59	19	3.4	176594	66	AC020983	AC020983	C	132	18	3.2	113547	62	AC011346	AC011346	Mus muscu
C	60	19	3.4	176530	78	AC087156	AC087156	C	133	18	3.2	115049	75	AC073746	AC073746	Mus muscu
C	61	19	3.4	179623	87	AC0113429	AC0113429	C	134	18	3.2	115049	75	AC073746	AC073746	Mus muscu
C	62	19	3.4	180493	62	AC011189	AC011189	C	135	18	3.2	115173	63	AC012612	AC012612	Mus muscu
C	63	19	3.4	182756	12	AC007789	AC007789	C	136	18	3.2	120397	76	AC079265	AC079265	Mus muscu
C	64	19	3.4	185171	68	AC023098	AC023098	C	137	18	3.2	120963	76	AC079482	AC079482	Mus muscu
C	65	19	3.4	194810	69	AC024984	AC024984	C	138	18	3.2	121063	76	AC079482	AC079482	Mus muscu
C	66	19	3.4	196530	83	CNS00YVI	AL096870	C	139	18	3.2	122049	92	HSB166C10	HSB166C10	Human DNA
C	67	19	3.4	199132	81	AL512631	AL512631	C	140	18	3.2	122326	77	AC079884	AC079884	Rattus no
C	68	19	3.4	203269	77	AC084876	AC084876	C	141	18	3.2	122326	77	AC079884	AC079884	Rattus no
C	69	19	3.4	204557	81	AL512585	AL512585	C	142	18	3.2	124236	14	IG002NM01	IG002NM01	Arabidops
C	70	19	3.4	208306	83	CNS01DSC	AL121767	C	143	18	3.2	132169	70	AC026814	AC026814	Mus muscu
C	71	19	3.4	210772	63	AC012215	AC012215	C	144	18	3.2	134350	85	AC004905	AC004905	Mus muscu
C	72	19	3.4	214159	83	CNS01DRT	AL118557	C	145	18	3.2	136662	85	AC005007	AC005007	Mus muscu
C	73	19	3.4	214241	77	AC084163	AC084163	C	146	18	3.2	137953	77	AC083888	AC083888	Rattus no
C	74	19	3.4	216315	92	HSG256022	AL080239	C	147	18	3.2	137953	77	AC083888	AC083888	Rattus no
C	75	19	3.4	226059	76	AC079488	AC079488	C	148	18	3.2	138970	70	AC026679	AC026679	Mus muscu
C	76	19	3.4	303041	67	AC029235	AC029235	C	149	18	3.2	141959	78	AC087130	AC087130	Mus muscu
C	77	19	3.4	306200	75	AP000991	AP000991	C	150	18	3.2	145976	87	AC018833	AC018833	Mus muscu
C	78	19	3.4	312615	75	AC073722	AC073722	C	151	18	3.2	147006	84	SPENUT904	SPENUT904	Staphyloc
C	79	19	3.4	340000	90	AP001697	AP001697	C	152	18	3.2	147744	61	AC008856	AC008856	Homo sapi
C	80	18	3.2	527	53	CNS01BHY	AL144455	C	153	18	3.2	148042	88	AC034426	AC034426	Homo sapi
C	81	18	3.2	1356	14	SCYLRO79W	Z73251	C	154	18	3.2	148648	73	AC068120	AC068120	Homo sapi
C	82	18	3.2	1798	12	AF033869	AF033869	C	155	18	3.2	149313	68	AC023548	AC023548	Homo sapi
C	83	18	3.2	2537	14	SCYLRO80W	Z73252	C	156	18	3.2	150695	68	AC023576	AC023576	Homo sapi
C	84	18	3.2	2845	94	AB023433	AB023433	C	157	18	3.2	151104	61	AC010250	AC010250	Homo sapi

c 158	18	3.2 151212	77	AC079885	AC079885	Rattus no	231	18	3.2 181596	74	AC069467	AC069467	Mus muscu
c 159	18	3.2 151788	78	AF321234	AF321234	Mus muscu	232	18	3.2 182421	65	AC016742	AC016742	Mus sapl
c 160	18	3.2 151959	62	AC011153	AC011153	Homo sapl	c 233	18	3.2 182982	72	AC036231	AC036231	Homo sapl
c 161	18	3.2 151979	69	AC025113	AC025113	Homo sapl	234	18	3.2 183042	81	AL445529	AL445529	Homo sapl
c 162	18	3.2 152468	82	AP001584	AP001584	Homo sapl	235	18	3.2 183936	94	AC007978	AC007978	Mus muscu
c 163	18	3.2 152544	68	AC023608	AC023608	Mus muscu	236	18	3.2 184000	64	AC016595	AC016595	Mus muscu
c 164	18	3.2 152742	67	AC022381	AC022381	Homo sapl	c 237	18	3.2 184166	71	AC027646	AC027646	Mus sapl
c 165	18	3.2 153027	71	AC027300	AC027300	Mus muscu	c 238	18	3.2 185351	87	AC015801	AC015801	Homo sapl
c 166	18	3.2 153258	70	AC026206	AC026206	Homo sapl	c 239	18	3.2 185462	78	AC087775	AC087775	Mus muscu
c 167	18	3.2 153233	70	AC026033	AC026033	Homo sapl	240	18	3.2 185548	94	AC005743	AC005743	Mus muscu
c 168	18	3.2 154704	2	AP000996	AP000996	Thermopla	c 241	18	3.2 185637	60	AC007979	AC007979	Mus muscu
c 169	18	3.2 155313	62	AC011091	AC011091	Homo sapl	242	18	3.2 186415	86	AC008675	AC008675	Mus muscu
c 170	18	3.2 155633	69	AC023510	AC023510	Homo sapl	c 243	18	3.2 186420	87	AC018757	AC018757	Homo sapl
c 171	18	3.2 155827	83	CNS05TC1	AL335099	Homo sapl	244	18	3.2 187376	73	AC068252	AC068252	Mus muscu
c 172	18	3.2 156266	13	AP002542	AP002542	Oryza sat	c 245	18	3.2 187376	94	AC078931	AC078931	Mus muscu
c 173	18	3.2 157180	14	NCB18D24	AL513466	Neurospor	c 246	18	3.2 189397	72	AC051643	AC051643	Mus muscu
c 174	18	3.2 157258	86	AC008379	AC008379	Homo sapl	c 247	18	3.2 190559	77	AC084164	AC084164	Mus sapl
c 175	18	3.2 157665	94	AC069018	AC069018	Mus muscu	248	18	3.2 190737	78	AL136158	AL136158	Mus muscu
c 176	18	3.2 157944	61	AC008788	AC008788	Homo sapl	c 249	18	3.2 191289	76	AC079290	AC079290	Mus muscu
c 177	18	3.2 158442	76	AC078920	AL335999	Homo sapl	c 250	18	3.2 191352	75	AC073565	AC073565	Mus muscu
c 178	18	3.2 158853	80	AL359999	AC036118	Homo sapl	251	18	3.2 191998	75	AC073869	AC073869	Homo sapl
c 179	18	3.2 160376	72	AC036118	AC032129	Homo sapl	252	18	3.2 192015	67	AC022453	AC022453	Mus muscu
c 180	18	3.2 161696	68	AC023129	AL365196	Homo sapl	c 253	18	3.2 193185	68	AC023606	AC023606	Mus muscu
c 181	18	3.2 163154	81	AL365196	AC016190	Homo sapl	c 254	18	3.2 193488	89	AL136097	AL136097	Human DNA
c 182	18	3.2 163328	64	AC016190	AC078896	Mus muscu	255	18	3.2 193636	76	AC079428	AC079428	Mus muscu
c 183	18	3.2 163449	76	AC078896	AC021628	Mus muscu	256	18	3.2 193708	76	AC074205	AC074205	Mus muscu
c 184	18	3.2 163860	67	AC021628	AC064640	Homo sapl	257	18	3.2 193907	78	AC087131	AC087131	Mus muscu
c 185	18	3.2 164119	70	AC026640	AC064801	Homo sapl	258	18	3.2 194262	81	AL450406	AL450406	Mus muscu
c 186	18	3.2 164682	73	AC064801	AC022011	Homo sapl	259	18	3.2 194394	72	AC040934	AC040934	Mus sapl
c 187	18	3.2 164816	67	AC022011	AC051613	Mus muscu	260	18	3.2 194476	75	AC074177	AC074177	Mus muscu
c 188	18	3.2 165372	72	AC051613	AL355498	Human DNA	c 261	18	3.2 194985	94	AC002406	AC002406	Mouse chr
c 189	18	3.2 165549	89	AL355498	AL500524	Homo sapl	262	18	3.2 195090	68	AC023150	AC023150	Homo sapl
c 190	18	3.2 165776	81	AL500524	AC073799	Mus muscu	263	18	3.2 195423	78	AC087151	AC087151	Mus muscu
c 191	18	3.2 166335	75	AC073799	AC008858	Homo sapl	264	18	3.2 196149	13	ANCHRY13	ANCHRY13	Mus muscu
c 192	18	3.2 167829	61	AC008858	AC018835	Homo sapl	c 265	18	3.2 197571	66	AC021042	AC021042	Mus sapl
c 193	18	3.2 167998	65	AC018835	AC026000	Homo sapl	266	18	3.2 198181	72	AC035248	AC035248	Mus muscu
c 194	18	3.2 168015	70	AC026000	AC022976	Homo sapl	c 267	18	3.2 198151	94	AF129005	AF129005	Mus muscu
c 195	18	3.2 168224	68	AC022976	AC036227	Homo sapl	268	18	3.2 198564	75	AC073939	AC073939	Mus muscu
c 196	18	3.2 168346	72	AC036227	AC079816	Mus muscu	269	18	3.2 198561	81	AL450395	AL450395	Mus muscu
c 197	18	3.2 168359	77	AC079816	AC078913	Mus muscu	c 270	18	3.2 199100	74	AC068902	AC068902	Mus muscu
c 198	18	3.2 168457	76	AC078913	AF259072	Mus muscu	c 271	18	3.2 199256	75	AC073553	AC073553	Mus muscu
c 199	18	3.2 170356	94	AF259072	AC068545	Homo sapl	c 272	18	3.2 199364	77	AC080064	AC080064	Mus sapl
c 200	18	3.2 170695	74	AC068545	AC068234	Homo sapl	c 273	18	3.2 200000	60	AC007117	AC007117	Mus sapl
c 201	18	3.2 172440	73	AC068234	AC011170	Homo sapl	274	18	3.2 200161	76	AC074313	AC074313	Mus muscu
c 202	18	3.2 173088	62	AC011170	AC027063	Homo sapl	c 275	18	3.2 200492	63	AL513217	AL513217	Mus sapl
c 203	18	3.2 173735	71	AC027063	AC06214	Homo sapl	c 276	18	3.2 200588	82	AL513206	AL513206	Homo sapl
c 204	18	3.2 174639	88	AC06214	AC087092	Homo sapl	c 277	18	3.2 201015	61	AC010075	AC010075	Homo sapl
c 205	18	3.2 174663	88	AC087092	AC027185	Mus muscu	278	18	3.2 201615	76	AC079274	AC079274	Mus sapl
c 206	18	3.2 175093	71	AC027185	AC068502	Mus muscu	279	18	3.2 202333	77	AC080144	AC080144	Mus muscu
c 207	18	3.2 175144	74	AC068502	AC079275	Mus muscu	280	18	3.2 202640	68	AC023234	AC023234	Mus muscu
c 208	18	3.2 175331	76	AC079275	AC020879	Mus muscu	c 281	18	3.2 202894	67	AC021630	AC021630	Mus muscu
c 209	18	3.2 176155	66	AC020879	AC079956	Mus muscu	282	18	3.2 202912	74	AC069560	AC069560	Mus muscu
c 210	18	3.2 176506	77	AC079956	AC026367	Homo sapl	c 283	18	3.2 203349	73	AC055819	AC055819	Mus muscu
c 211	18	3.2 176564	70	AC026367	AC026335	Homo sapl	c 284	18	3.2 203959	90	AP001137	AP001137	Mus muscu
c 212	18	3.2 176853	70	AC026335	AC019351	Homo sapl	285	18	3.2 204056	89	AL160397	AL160397	Human DNA
c 213	18	3.2 177130	66	AC019351	AC079217	Homo sapl	286	18	3.2 205104	81	AL1391989	AL1391989	Homo sapl
c 214	18	3.2 177205	76	AC079217	AC074129	Homo sapl	287	18	3.2 205677	74	AC068651	AC068651	Mus muscu
c 215	18	3.2 177663	75	AC074129	AC074129	Homo sapl	c 288	18	3.2 205959	67	AC022328	AC022328	Mus muscu
c 216	18	3.2 177663	75	AC074129	AC016844	Homo sapl	c 289	18	3.2 205992	72	AC044811	AC044811	Mus sapl
c 217	18	3.2 177751	65	AC016844	AC026384	Mus muscu	c 290	18	3.2 206383	94	AC008160	AC008160	Mus muscu
c 218	18	3.2 177767	70	AC026384	AC010411	Homo sapl	c 291	18	3.2 206703	77	AC083909	AC083909	Mus muscu
c 219	18	3.2 177767	70	AC026384	AC080141	Mus muscu	c 292	18	3.2 206703	77	AC083909	AC083909	Mus muscu
c 220	18	3.2 177803	87	AC010411	AC080141	Mus muscu	293	18	3.2 207607	75	AC073590	AC073590	Mus muscu
c 221	18	3.2 177914	87	AC080141	AC008770	Homo sapl	294	18	3.2 207949	71	AC027497	AC027497	Homo sapl
c 222	18	3.2 178180	77	AC008770	AL137069	Homo sapl	295	18	3.2 208211	77	AC084287	AC084287	Mus muscu
c 223	18	3.2 178509	78	AL137069	AC069149	Homo sapl	c 296	18	3.2 208211	77	AC084287	AC084287	Mus muscu
c 224	18	3.2 179272	74	AC069149	AL512586	Mus muscu	c 297	18	3.2 208295	69	AC025528	AC025528	Mus muscu
c 225	18	3.2 179432	81	AL512586	AC026683	Mus muscu	298	18	3.2 208405	81	AL365219	AL365219	Homo sapl
c 226	18	3.2 179493	70	AC026683	AC009397	Homo sapl	299	18	3.2 208910	76	AC079573	AC079573	Mus muscu
c 227	18	3.2 179581	61	AC009397	AC083884	Homo sapl	c 300	18	3.2 208910	76	AC079573	AC079573	Mus muscu
c 228	18	3.2 180548	77	AC083884	AC079219	Mus muscu	c 301	18	3.2 208932	76	AC074329	AC074329	Mus muscu
c 229	18	3.2 181008	76	AC079219	AL161725	Human DNA	c 302	18	3.2 209301	76	AC079529	AC079529	Mus muscu
c 230	18	3.2 181179	89	AL161725			303	18	3.2 211600	63	AC013266	AC013266	Homo sapl

304	18	3.2	211615	71	AC026949	Mus muscu	377	17	3.1	816	14	CRPSAH	X15164 C.reinhardt
305	18	3.2	212437	76	AL354924	Homo sapi	378	17	3.1	902	53	CNS01R72	AL457038 Anopheles
306	18	3.2	212668	79	AC079426	Mus muscu	379	17	3.1	1011	53	CNS0719P	AL42643 T3 end of
307	18	3.2	213396	73	AC067784	Homo sapi	380	17	3.1	1147	75	AC073605	AC023605 Homo sapi
308	18	3.2	213308	76	AC079164	Mus muscu	381	17	3.1	1160	89	AK026210	AK026210 Homo sapi
309	18	3.2	213318	72	AC036121	Mus muscu	382	17	3.1	1121	89	AK021466	AK021466 Homo sapi
310	18	3.2	214157	76	AC079511	Mus muscu	383	17	3.1	1160	9	AX028832	AX028832 Sequence
311	18	3.2	214157	76	AC079511	Mus muscu	384	17	3.1	1255	11	PT4DDAA	J05172 Bacteriophage
312	18	3.2	214707	73	AC073945	Mus muscu	385	17	3.1	2368	94	PSAPSPYN2	Y13322 Plasmid
313	18	3.2	215309	75	AC060761	Mus muscu	386	17	3.1	2426	89	MMU251508	Y13525 Plasmid
314	18	3.2	216101	81	AL450331	Mus muscu	387	17	3.1	2426	89	AK026452	AK026452 Homo sapi
315	18	3.2	216340	75	AC073754	Mus muscu	388	17	3.1	2590	7	AF222767	AF222767 Homo sapi
316	18	3.2	216583	78	AC087166	Mus muscu	389	17	3.1	2674	93	SSCFMR7	SSCFMR7 Bos lauru
317	18	3.2	217250	65	AC018595	Homo sapi	390	17	3.1	2676	92	HSMB01876	HSMB01876 Homo sapi
318	18	3.2	218907	78	AC087558	Mus muscu	391	17	3.1	3263	6	PSAD1	PSAD1 X06281 Pea mRNA
319	18	3.2	220469	76	AC074307	Mus muscu	392	17	3.1	4011	14	AF221497	AF221497 Gossypium
320	18	3.2	221111	76	AC079526	Mus muscu	393	17	3.1	4055	13	CBORNTF	CBORNTF X6262 C.barati ge
321	18	3.2	221285	68	AC023611	Mus muscu	394	17	3.1	4073	2	HUM21DC922	HUM21DC922 Homo sapien
322	18	3.2	221478	76	AC079545	Mus muscu	395	17	3.1	4148	93	SYPSAAB	SYPSAAB X58825 Synecocyst
323	18	3.2	222468	76	AC079525	Mus muscu	396	17	3.1	4938	4	AE002878	AE002878 Drosophila
324	18	3.2	222468	76	AC079525	Mus muscu	397	17	3.1	6536	4	AB007967	AB007967 Homo sapi
325	18	3.2	222658	94	AC055766	Mus muscu	398	17	3.1	6731	85	CEC13E3	CEC13E3 U40936 Caenorhabdit
326	18	3.2	222707	76	AC079425	Mus muscu	399	17	3.1	6850	58	ECR5695	ECR5695 A005695 Echovirus
327	18	3.2	226168	94	AC078930	Mus muscu	400	17	3.1	7248	58	AF003255	AF003255 Mus muscu
328	18	3.2	228667	81	AL365336	Mus muscu	401	17	3.1	7721	94	AB007122	AB007122 Arthropod
329	18	3.2	228789	72	AC051638	Mus muscu	402	17	3.1	7764	66	AC019416	AC019416 Drosophila
330	18	3.2	229010	75	AC073686	Mus muscu	403	17	3.1	8127	1	AB007122	AB007122 Arthropod
331	18	3.2	229010	75	AC073686	Mus muscu	404	17	3.1	8682	14	C1P345R5S	C1P345R5S U39682 Mycoplasma
332	18	3.2	230693	80	AL359352	Mus muscu	405	17	3.1	10563	3	U39682	U39682 Mycoplasma
333	18	3.2	231709	74	AC068561	Mus muscu	406	17	3.1	11198	1	AE006271	AE006271 Lactococcus
334	18	3.2	234257	76	AC079574	Mus muscu	407	17	3.1	11261	93	HSMP03	HSMP03 X6088 Human perio
335	18	3.2	234411	94	MMU2971	Mus muscu	408	17	3.1	11698	2	KOCYMSCGT	KOCYMSCGT X86014 K.oxyloca c
336	18	3.2	239423	77	AC083912	Mus muscu	409	17	3.1	15121	6	LMFL6754	LMFL6754 AL358632 Leishman
337	18	3.2	240622	75	AC073793	Mus muscu	410	17	3.1	15859	5	CEFD7D3	CEFD7D3 AC017212 Drosophila
338	18	3.2	244110	82	AL513022	Mus muscu	411	17	3.1	20981	65	AC017212	AC017212 Drosophila
339	18	3.2	244215	75	AC073706	Mus muscu	412	17	3.1	26147	6	CEC13E3	CEC13E3 Z93395 Caenorhabdit
340	18	3.2	244215	75	AC073706	Mus muscu	413	17	3.1	26703	5	CBRG45011	CBRG45011 AC084652 Caenorhab
341	18	3.2	245156	77	AC084021	Mus muscu	414	17	3.1	26767	6	CELM07G9	CELM07G9 AF040658 Caenorhab
342	18	3.2	246823	76	AC079483	Mus muscu	415	17	3.1	32410	90	AP000164	AP000164 Homo sapi
343	18	3.2	251216	76	AC079558	Mus muscu	416	17	3.1	32588	6	CEY22FE5A	CEY22FE5A AL021479 Caenorhab
344	18	3.2	251216	76	AC079558	Mus muscu	417	17	3.1	34338	66	AC020840	AC020840 Mus muscu
345	18	3.2	252504	75	AC073815	Mus muscu	418	17	3.1	35740	88	AF199339	AF199339 Homo sapi
346	18	3.2	254475	69	AC025117	Mus muscu	419	17	3.1	36080	6	CER10D12	CER10D12 Z81109 Caenorhabdit
347	18	3.2	256673	78	AC087146	Mus muscu	420	17	3.1	36092	93	HSU73640	HSU73640 Human chrom
348	18	3.2	258088	75	AC073766	Mus muscu	421	17	3.1	38591	5	CEC54E10	CEC54E10 Z81487 Caenorhabdit
349	18	3.2	262205	74	AE003647	Mus muscu	422	17	3.1	40033	91	HS1110P6	HS1110P6 AL049475 Human DNA
350	18	3.2	265233	94	AC012382	Mus muscu	423	17	3.1	40289	92	CEY48610A	CEY48610A AL132847 Caenorhab
351	18	3.2	291768	76	AC074229	Mus muscu	424	17	3.1	42807	92	HS1309F20	HS1309F20 AL112917 Human DNA
352	18	3.2	292943	68	AC023605	Mus muscu	425	17	3.1	43051	85	AB001517	AB001517 Homo sapi
353	18	3.2	292943	68	AC023605	Mus muscu	426	17	3.1	43125	5	AF147779	AF147779 AF147779 Drosophila
354	18	3.2	293184	76	AC079487	Mus muscu	427	17	3.1	44499	12	AB016876	AB016876 Arabidops
355	18	3.2	299974	76	AC079512	Mus muscu	428	17	3.1	45794	64	AC015492	AC015492 Homo sapi
356	18	3.2	300250	94	AF125314	Mus muscu	429	17	3.1	46778	77	AC079784	AC079784 Homo sapi
357	18	3.2	303249	4	AE001515	Mus muscu	430	17	3.1	47743	5	CEIC06E2	CEIC06E2 U39674 Caenorhabdit
358	18	3.2	304383	4	AE003579	Mus muscu	431	17	3.1	48008	12	AB025621	AB025621 Arabidops
359	18	3.2	304407	75	AC073813	Mus muscu	432	17	3.1	48823	65	AC017217	AC017217 Drosophila
360	18	3.2	307380	78	AC087155	Mus muscu	433	17	3.1	50191	90	AL450471	AL450471 Human DNA
361	18	3.2	312430	75	AC073722	Mus muscu	434	17	3.1	52290	69	AC025314	AC025314 Homo sapi
362	18	3.2	312615	75	AC073722	Mus muscu	435	17	3.1	53444	66	AC019747	AC019747 Drosophila
363	18	3.2	316756	65	DROSADH06	Mus muscu	436	17	3.1	53635	78	AC087498	AC087498 Homo sapi
364	18	3.2	318503	75	AC074166	Mus muscu	437	17	3.1	57186	85	AC004042	AC004042 Homo sapi
365	18	3.2	331339	66	AC020958	Mus muscu	438	17	3.1	60309	78	AL138922	AL138922 Homo sapi
366	18	3.2	340000	90	AE001681	Mus muscu	439	17	3.1	63442	66	AC020280	AC020280 Drosophila
367	17	3.1	299	54	G26916	Homo sapi	440	17	3.1	65771	63	AL135782	AL135782 Homo sapi
368	17	3.1	388	5	AF058227	Scutellaria	441	17	3.1	65771	63	AL135782	AL135782 Homo sapi
369	17	3.1	393	5	AF072664	Scutellaria	442	17	3.1	65971	91	HS892F13	HS892F13 Human DNA
370	17	3.1	431	54	G42233	Mycoplasma	443	17	3.1	66452	63	AC013231	AC013231 Drosophila
371	17	3.1	652	2	MGU02253	Mycoplasma	444	17	3.1	66452	63	AC013231	AC013231 Drosophila
372	17	3.1	652	2	MGU02253	Mycoplasma	445	17	3.1	66806	90	AF000022	AF000022 Homo sapi
373	17	3.1	660	14	CNS01C02	Mycoplasma	446	17	3.1	67249	65	AC018611	AC018611 Homo sapi
374	17	3.1	720	14	CNS01C03	Mycoplasma	447	17	3.1	69463	77	AC084249	AC084249 Homo sapi
375	17	3.1	777	10	EL16701	gDNA encodi	448	17	3.1	69614	77	AC083925	AC083925 Homo sapi
376	17	3.1	785	53	CNS077FM	gDNA encodi	449	17	3.1	69714	69	AC024143	AC024143 Mus muscu

450	17	3.1	70768	12	AC007069	AC007069 Arabidops	523	17	3.1	114521	89	AL159985	AL159985 Human DNA
451	17	3.1	71801	79	AL353613	Continuation (4 of	524	17	3.1	115039	91	HS14558	AL035451 Human DNA
452	17	3.1	73166	77	AC083961	AC083961 Homo sapi	525	17	3.1	117553	82	AP000595	AP000595 Homo sapi
453	17	3.1	73639	73	AC055834	AC055834 Homo sapi	526	17	3.1	117937	78	AL139146	AL139146 Homo sapi
454	17	3.1	73947	90	AL445248	AL445248 Homo sapi	527	17	3.1	118421	82	AL151322	AL151322 Homo sapi
455	17	3.1	76339	89	AL157694	AL157694 Human DNA	528	17	3.1	119072	89	AL136531	AL136531 Human DNA
456	17	3.1	77223	90	AL360180	AL360180 Human DNA	529	17	3.1	120400	78	AL139106	AL139106 Homo sapi
457	17	3.1	78373	70	AC026519	AC026519 Homo sapi	530	17	3.1	120507	89	AL136358	AL136358 Human DNA
458	17	3.1	78373	70	AC026519	AC026519 Homo sapi	531	17	3.1	123010	61	AC009746	AC009746 Homo sapi
459	17	3.1	79134	67	AC021771	AC021771 Homo sapi	532	17	3.1	123323	90	AP001816	AP001816 Drosophill
460	17	3.1	79725	12	AC003105	AC003105 Arabidops	533	17	3.1	124343	76	AC079188	AC079188 Homo sapi
461	17	3.1	80201	61	AC009015	AC009015 Homo sapi	534	17	3.1	125441	61	AC008902	AC008902 Homo sapi
462	17	3.1	81266	12	AC006920	AC006920 Arabidops	535	17	3.1	125536	60	AC008302	AC008302 Homo sapi
463	17	3.1	81524	92	HSJ49616	ALJ009616 Homo sapi	536	17	3.1	126244	80	AL156779	AL156779 Homo sapi
464	17	3.1	82213	79	AL162264	AL162264 Homo sapi	537	17	3.1	126781	64	AC016373	AC016373 Homo sapi
465	17	3.1	82381	13	ATF27619	AL078467 Arabidops	538	17	3.1	126814	61	AC008961	AC008961 Homo sapi
466	17	3.1	83057	90	AL445703	AL445703 Human DNA	539	17	3.1	126910	86	AC005856	AC005856 Homo sapi
467	17	3.1	83351	12	AC010657	AC010657 Genomic s	540	17	3.1	127413	89	AL137784	AL137784 Human DNA
468	17	3.1	83369	13	ATT30A10	AL117386 Arabidops	541	17	3.1	127646	86	AC008171	AC008171 Homo sapi
469	17	3.1	83371	13	ATTM4122	AL030978 Arabidops	542	17	3.1	127926	61	AC010337	AC010337 Homo sapi
470	17	3.1	83689	12	AB017067	AB017067 Arabidops	543	17	3.1	128265	60	AC007826	AC007826 Homo sapi
471	17	3.1	84371	82	AP001963	AP001963 Homo sapi	544	17	3.1	128921	88	AC068658	AC068658 Homo sapi
472	17	3.1	85559	68	AC022892	AC022892 Homo sapi	545	17	3.1	130177	92	HSBG279B7	HSBG279B7 Homo sapi
473	17	3.1	85757	4	AC001652	AC001652 Drosophill	546	17	3.1	131355	78	AC089989	AC089989 Ratius no
474	17	3.1	86671	12	AC005724	AC005724 Arabidops	547	17	3.1	133258	85	AC004944	AC004944 Homo sapi
475	17	3.1	87100	91	HSJ38L4	Z97635 Human DNA s	548	17	3.1	133478	85	AC004686	AC004686 Homo sapi
476	17	3.1	87114	85	AC005353	AC005353 Homo sapi	549	17	3.1	133787	87	AC015540	AC015540 Homo sapi
477	17	3.1	87306	78	AF205591	AF205591 Homo sapi	550	17	3.1	134189	76	AC079550	AC079550 Homo sapi
478	17	3.1	87402	90	AP001426	AP001426 Homo sapi	551	17	3.1	134515	91	HS354U5	HS354U5 Homo sapi
479	17	3.1	87619	64	AC016504	AC016504 Homo sapi	552	17	3.1	134649	85	AC004047	AC004047 Homo sapi
480	17	3.1	87925	85	AC005318	AC005318 Homo sapi	553	17	3.1	135095	77	AC084714	AC084714 Homo sapi
481	17	3.1	89319	92	HSBK29F11	AL118516 Human DNA	554	17	3.1	135176	75	AC073907	AC073907 Homo sapi
482	17	3.1	89453	12	AC068655	AC068655 Genomic S	555	17	3.1	135551	2	D90906	D90906 Synchocyst
483	17	3.1	90448	12	AC079730	AC079730 Arabidops	556	17	3.1	137159	74	AC069090	AC069090 Homo sapi
484	17	3.1	90448	12	AC079733	AC079733 Arabidops	557	17	3.1	137304	86	AC005627	AC005627 Homo sapi
485	17	3.1	90604	86	AC006525	AC006525 Homo sapi	558	17	3.1	137557	86	AC005909	AC005909 Homo sapi
486	17	3.1	91331	82	AP001970	AP001970 Homo sapi	559	17	3.1	137720	85	AC005410	AC005410 Homo sapi
487	17	3.1	91549	76	AC079339	AC079339 Homo sapi	560	17	3.1	137794	65	AC016854	AC016854 Homo sapi
488	17	3.1	93848	80	AL356501	AL356501 Homo sapi	561	17	3.1	138490	94	MMJ249895	MMJ249895 Mus muscu
489	17	3.1	95096	86	AC008384	AC008384 Homo sapi	562	17	3.1	138909	62	AC010612	AC010612 Homo sapi
490	17	3.1	95614	63	AC012890	AC012890 Drosophill	563	17	3.1	138909	90	CNS01D53	AL121653 BAC seque
491	17	3.1	96109	10	AX067460	AX067460 Sequence	564	17	3.1	138912	79	AL160257	AL160257 Homo sapi
492	17	3.1	96276	92	HSJ117516	AL049538 Human DNA	565	17	3.1	139301	80	AL359971	AL359971 Homo sapi
493	17	3.1	97176	78	AL139249	AL139249 Homo sapi	566	17	3.1	139338	83	AP002879	AP002879 Homo sapi
494	17	3.1	97454	89	AL139147	AL139147 Human DNA	567	17	3.1	139467	6	D90905	D90905 Synchocyst
495	17	3.1	98219	85	AC005282	AC005282 Homo sapi	568	17	3.1	140000	66	AC019064	AC019064 Homo sapi
496	17	3.1	99075	78	AF186996	AF186996 Homo sapi	569	17	3.1	140136	89	AL136087	AL136087 Human DNA
497	17	3.1	99358	89	AL137858	AL137858 Human DNA	570	17	3.1	140357	64	AC016221	AC016221 Homo sapi
498	17	3.1	100269	91	HS105C14	AL049610 Human DNA	571	17	3.1	140730	90	AP001960	AP001960 Homo sapi
499	17	3.1	101615	85	AC004038	AC004038 Homo sapi	572	17	3.1	140852	61	AC009734	AC009734 Drosophill
500	17	3.1	106117	82	AP000628	AP000628 Homo sapi	573	17	3.1	141103	81	AL445241	AL445241 Homo sapi
501	17	3.1	106988	85	AC001226	AC001226 Genomic s	574	17	3.1	142055	62	AC010495	AC010495 Homo sapi
502	17	3.1	107681	85	AC005476	AC005476 Homo sapi	575	17	3.1	142103	81	AL390863	AL390863 Homo sapi
503	17	3.1	107728	79	AL162721	AL162721 Homo sapi	576	17	3.1	142509	74	AC068571	AC068571 Homo sapi
504	17	3.1	108040	73	AC068150	AC068150 Homo sapi	577	17	3.1	142908	82	AL513172	AL513172 Homo sapi
505	17	3.1	109173	86	AC007678	AC007678 Homo sapi	578	17	3.1	143892	92	HSJ2680N4	HSJ2680N4 Homo sapi
506	17	3.1	109201	85	AC000403	AC000403 Genomic s	579	17	3.1	143894	74	AC069002	AC069002 Homo sapi
507	17	3.1	109723	78	AF165146	AF165146 Homo sapi	580	17	3.1	144013	69	AC025059	AC025059 Homo sapi
508	17	3.1	110000	60	AC003656	Continuation (6 of	581	17	3.1	144234	83	AP002425	AP002425 Homo sapi
509	17	3.1	110000	60	AC003656	Continuation (7 of	582	17	3.1	144279	82	AP001570	AP001570 Homo sapi
510	17	3.1	110000	60	AC007194	Continuation (2 of	583	17	3.1	144348	64	AC016423	AC016423 Homo sapi
511	17	3.1	110000	64	AC016584	AC016584 Homo sapi	584	17	3.1	144391	73	AC055823	AC055823 Homo sapi
512	17	3.1	110000	80	AL357125	Continuation (2 of	585	17	3.1	144410	68	AC023992	AC023992 Homo sapi
513	17	3.1	110000	81	AL390202	Continuation (9 of	586	17	3.1	145231	74	AC068992	AC068992 Homo sapi
514	17	3.1	110000	83	CER48G10	AL021450 Caenorh	587	17	3.1	145239	82	AP000653	AP000653 Homo sapi
515	17	3.1	110000	83	CER54E2	Continuation (2 of	588	17	3.1	145485	64	AC016533	AC016533 Homo sapi
516	17	3.1	111566	12	AC000348	AC000348 Genomic s	589	17	3.1	145767	62	AC011094	AC011094 Homo sapi
517	17	3.1	111351	87	AC001484	AC001484 Homo sapi	590	17	3.1	145846	66	AC020298	AC020298 Drosophill
518	17	3.1	112632	78	AL137158	AL137158 Homo sapi	591	17	3.1	145871	90	AL391601	AL391601 Human DNA
519	17	3.1	112632	78	AL137158	AL137158 Homo sapi	592	17	3.1	146059	65	AC019030	AC019030 Homo sapi
520	17	3.1	112902	85	AC005230	AC005230 Homo sapi	593	17	3.1	146077	68	AC023380	AC023380 Homo sapi
521	17	3.1	113280	81	AL390236	AL390236 Homo sapi	594	17	3.1	146420	80	AL358875	AL358875 Homo sapi
522	17	3.1	113826	89	AL133378	AL133378 Human DNA	595	17	3.1	146691	83	AP002402	AP002402 Homo sapi

C 596	17	3.1 146831	91	HS523C21	AL021408 Homo sapi	669	17	3.1 160168	91	CNS05TDH	AL356799 Human chr
C 597	17	3.1 147174	13	AP000492	AP000492 Oryza sat	670	17	3.1 160225	72	AC037438	AC037438 Homo sapi
C 598	17	3.1 147240	79	AL353720	Homo sapi	671	17	3.1 160436	73	AC067855	AC067855 Homo sapi
C 599	17	3.1 147448	63	AC012272	AC012272 Homo sapi	672	17	3.1 160480	12	AF123535	AF123535 Zea mays
C 600	17	3.1 147712	87	AC011299	AC011299 Homo sapi	673	17	3.1 160589	69	AC025149	AC025149 Homo sapi
C 601	17	3.1 147847	82	AL513213	AL513213 Homo sapi	674	17	3.1 160583	62	NC010968	NC010968 Homo sapi
C 602	17	3.1 148191	80	AL356391	Homo sapi	675	17	3.1 161192	66	AC020720	AC020720 Homo sapi
C 603	17	3.1 148400	79	AL354749	AL354749 Homo sapi	676	17	3.1 161346	81	AL391864	AL391864 Homo sapi
C 604	17	3.1 148583	83	CEV11D7	Z92818 Caenorhabdi	677	17	3.1 161596	76	AC079586	AC079586 Homo sapi
C 605	17	3.1 148595	72	AC036129	AC036129 Homo sapi	678	17	3.1 161906	71	AC027206	AC027206 Homo sapi
C 606	17	3.1 149087	89	AL157826	AL157826 Human DNA	679	17	3.1 162002	67	AC022697	AC022697 Homo sapi
C 607	17	3.1 149101	74	AC069375	AC069375 Homo sapi	680	17	3.1 162237	89	AL133549	AL133549 Human DNA
C 608	17	3.1 149124	78	AL136079	AL136079 Homo sapi	681	17	3.1 162354	75	AC073299	AC073299 Homo sapi
C 609	17	3.1 149220	68	AC022539	AC022539 Homo sapi	682	17	3.1 162463	80	AL359760	AL359760 Homo sapi
C 610	17	3.1 149607	67	AC022109	AC022109 Homo sapi	683	17	3.1 162493	74	AC068776	AC068776 Homo sapi
C 611	17	3.1 149919	67	AC022545	AC022545 Homo sapi	684	17	3.1 162590	72	AC036203	AC036203 Homo sapi
C 612	17	3.1 150027	64	AC015596	AC015596 Homo sapi	685	17	3.1 162695	89	AL353580	AL353580 Homo sapi
C 613	17	3.1 150902	68	AC023106	AC023106 Homo sapi	686	17	3.1 162731	74	AC068326	AC068326 Homo sapi
C 614	17	3.1 151073	88	AC073141	AC073141 Homo sapi	687	17	3.1 162764	70	AC026063	AC026063 Homo sapi
C 615	17	3.1 151879	80	AL355813	AL355813 Homo sapi	688	17	3.1 162775	64	AC015896	AC015896 Homo sapi
C 616	17	3.1 152103	63	AC012130	AC012130 Homo sapi	689	17	3.1 162912	92	HSAC002067	HSAC002067
C 617	17	3.1 153141	73	AC062021	AC062021 Homo sapi	690	17	3.1 162968	79	AL354978	AL354978 Homo sapi
C 618	17	3.1 153364	61	AC009787	AC009787 Homo sapi	691	17	3.1 162975	69	AC025225	AC025225 Homo sapi
C 619	17	3.1 153463	69	AC024643	AC024643 Homo sapi	692	17	3.1 162993	82	AP000889	AP000889 Homo sapi
C 620	17	3.1 153946	60	AC008673	AC008673 Homo sapi	693	17	3.1 163268	66	NC019159	NC019159 Homo sapi
C 621	17	3.1 154353	61	NC010472	NC010472 Homo sapi	694	17	3.1 163712	85	AC010465	AC010465 Homo sapi
C 622	17	3.1 154453	62	AC011179	AC011179 Homo sapi	695	17	3.1 163929	71	AC027686	AC027686 Homo sapi
C 623	17	3.1 154561	13	AP002819	AP002819 Oryza sat	696	17	3.1 164112	75	AC073193	AC073193 Homo sapi
C 624	17	3.1 154666	69	AC025182	AC025182 Homo sapi	697	17	3.1 164229	86	AC006386	AC006386 Homo sapi
C 625	17	3.1 154784	69	AC025362	AC025362 Homo sapi	698	17	3.1 164286	77	NC079839	NC079839 Homo sapi
C 626	17	3.1 154796	86	AC007372	AC007372 Homo sapi	699	17	3.1 164309	73	AC067834	AC067834 Homo sapi
C 627	17	3.1 154825	72	NC053517	NC053517 Homo sapi	700	17	3.1 164354	77	AC064811	AC064811 Homo sapi
C 628	17	3.1 154923	78	AL138781	AL138781 Homo sapi	701	17	3.1 164604	74	AC027383	AC027383 Homo sapi
C 629	17	3.1 155146	69	AC025216	AC025216 Homo sapi	702	17	3.1 164719	74	AC068623	AC068623 Homo sapi
C 630	17	3.1 155436	73	AC009666	AC009666 Homo sapi	703	17	3.1 164798	62	AC010651	AC010651 Homo sapi
C 631	17	3.1 155779	61	AC068260	AC068260 Homo sapi	704	17	3.1 164833	69	AC024296	AC024296 Homo sapi
C 632	17	3.1 155808	65	NC018956	NC018956 Homo sapi	705	17	3.1 164924	79	AL354941	AL354941 Homo sapi
C 633	17	3.1 155941	76	NC079211	NC079211 Homo sapi	706	17	3.1 164942	69	AC024656	AC024656 Homo sapi
C 634	17	3.1 156361	70	AC026174	AC026174 Homo sapi	707	17	3.1 165190	81	AL390788	AL390788 Homo sapi
C 635	17	3.1 156378	77	AC084267	AC084267 Homo sapi	708	17	3.1 165711	62	AC011884	AC011884 Homo sapi
C 636	17	3.1 156681	67	AC022418	AC022418 Homo sapi	709	17	3.1 165901	94	MM437P9	MM437P9 Mus muscu
C 637	17	3.1 156776	70	AC026528	AC026528 Homo sapi	710	17	3.1 166197	75	AC073552	AC073552 Homo sapi
C 638	17	3.1 156783	69	AC025482	AC025482 Homo sapi	711	17	3.1 166234	91	HS273P12	HS273P12 Homo sapi
C 639	17	3.1 156838	76	NC078862	NC078862 Homo sapi	712	17	3.1 166272	60	AC007841	AC007841 Homo sapi
C 640	17	3.1 156955	61	AC009419	AC009419 Homo sapi	713	17	3.1 166344	79	AL162577	AL162577 Homo sapi
C 641	17	3.1 157007	90	CNS01DX7	AL139099 Human chr	714	17	3.1 166819	83	CEY22F5	CEY22F5 Caenorhabdi
C 642	17	3.1 157051	62	AC011095	AC011095 Homo sapi	715	17	3.1 166862	74	AC069533	AC069533 Homo sapi
C 643	17	3.1 157122	77	AC087109	AC087109 Homo sapi	716	17	3.1 166966	78	AL138685	AL138685 Homo sapi
C 644	17	3.1 157348	83	AP002446	AP002446 Homo sapi	717	17	3.1 167025	90	AL445439	AL445439 Homo sapi
C 645	17	3.1 157393	72	NC036212	NC036212 Homo sapi	718	17	3.1 167257	86	AC008008	AC008008 Homo sapi
C 646	17	3.1 157611	72	AC040910	AC040910 Homo sapi	719	17	3.1 167441	75	AC073832	AC073832 Homo sapi
C 647	17	3.1 157613	87	AC018769	AC018769 Homo sapi	720	17	3.1 167494	82	AP002088	AP002088 Homo sapi
C 648	17	3.1 157769	76	AC074193	AC074193 Homo sapi	721	17	3.1 167571	71	AC027761	AC027761 Homo sapi
C 649	17	3.1 157889	77	AC079996	AC079996 Homo sapi	722	17	3.1 167700	86	AC007036	AC007036 Homo sapi
C 650	17	3.1 157903	13	AP000570	AP000570 Oryza sat	723	17	3.1 167721	71	AC032019	AC032019 Homo sapi
C 651	17	3.1 158019	79	AL354774	AL354774 Homo sapi	724	17	3.1 167803	62	AC010816	AC010816 Homo sapi
C 652	17	3.1 158116	80	AL357622	AL357622 Homo sapi	725	17	3.1 167830	66	AC020678	AC020678 Homo sapi
C 653	17	3.1 158207	67	AC021942	AC021942 Homo sapi	726	17	3.1 167830	71	AC027768	AC027768 Homo sapi
C 654	17	3.1 158334	70	AC025858	AC025858 Homo sapi	727	17	3.1 168475	64	AC015698	AC015698 Homo sapi
C 655	17	3.1 158280	62	AC011087	AC011087 Homo sapi	728	17	3.1 167886	80	AL359260	AL359260 Homo sapi
C 656	17	3.1 158483	70	AC025987	AC025987 Homo sapi	729	17	3.1 167932	73	AC068133	AC068133 Homo sapi
C 657	17	3.1 158714	12	NC082644	NC082644 Oryza sat	730	17	3.1 168079	69	AC024709	AC024709 Homo sapi
C 658	17	3.1 158905	86	AC005666	AC005666 Homo sapi	731	17	3.1 168247	83	AC005014	AC005014 Homo sapi
C 659	17	3.1 159487	81	AL441963	AL441963 Homo sapi	732	17	3.1 168362	65	AC012413	AC012413 Homo sapi
C 660	17	3.1 159577	77	AC080060	AC080060 Homo sapi	733	17	3.1 168475	78	AC015698	AC015698 Homo sapi
C 661	17	3.1 159612	74	AC069095	AC069095 Homo sapi	734	17	3.1 168677	90	CNS0000F	CNS0000F Human chr
C 662	17	3.1 159725	76	AC079320	AC079320 Homo sapi	735	17	3.1 168803	11	AF158101	AF158101 Homo sapi
C 663	17	3.1 159777	78	AF306443	AF306443 Homo sapi	736	17	3.1 169172	70	AL356799	AL356799 Homo sapi
C 664	17	3.1 159824	79	AL353649	AL353649 Homo sapi	737	17	3.1 169184	90	AL356969	AL356969 Homo sapi
C 665	17	3.1 159857	87	AC018767	AC018767 Homo sapi	738	17	3.1 169299	62	AC011750	AC011750 Homo sapi
C 666	17	3.1 159976	64	AC016124	AC016124 Homo sapi	739	17	3.1 169362	78	AL136440	AL136440 Homo sapi
C 667	17	3.1 160007	74	AC068892	AC068892 Homo sapi	740	17	3.1 169515	68	AC023213	AC023213 Homo sapi
C 668	17	3.1 160112	72	NC046171	NC046171 Homo sapi	741	17	3.1 169516	63	AC013934	AC013934 Drosophila

742	17	3.1.169610	79	AL354854	AL354854 Homo sapi	C 815	17	3.1.178367	64	AC015614	AC015614 Homo sapi	815	17	3.1.178367	64	AC015614	AC015614 Homo sapi
743	17	3.1.169700	60	AC008437	AC008437 Homo sapi	C 816	17	3.1.178443	75	AC073348	AC073348 Homo sapi	816	17	3.1.178443	75	AC073348	AC073348 Homo sapi
744	17	3.1.169884	66	AC020596	AC020596 Homo sapi	C 817	17	3.1.178632	80	AL359998	AL359998 Homo sapi	817	17	3.1.178632	80	AL359998	AL359998 Homo sapi
745	17	3.1.170064	68	AC022771	AC022771 Homo sapi	C 818	17	3.1.178929	90	AL359252	AL359252 Homo sapi	818	17	3.1.178929	90	AL359252	AL359252 Homo sapi
746	17	3.1.170189	71	AC027615	AC027615 Homo sapi	C 819	17	3.1.179075	65	AC018518	AC018518 Homo sapi	819	17	3.1.179075	65	AC018518	AC018518 Homo sapi
747	17	3.1.170218	73	AC068125	AC068125 Homo sapi	C 820	17	3.1.179162	82	AP001823	AP001823 Homo sapi	820	17	3.1.179162	82	AP001823	AP001823 Homo sapi
748	17	3.1.170402	77	AC080097	AC080097 Homo sapi	C 821	17	3.1.179207	61	AC009900	AC009900 Homo sapi	821	17	3.1.179207	61	AC009900	AC009900 Homo sapi
749	17	3.1.170421	79	AC080097	AC080097 Homo sapi	C 822	17	3.1.179518	76	AC079203	AC079203 Homo sapi	822	17	3.1.179518	76	AC079203	AC079203 Homo sapi
750	17	3.1.170452	88	AF152364	AF152364 Homo sapi	C 823	17	3.1.179561	86	AC006433	AC006433 Homo sapi	823	17	3.1.179561	86	AC006433	AC006433 Homo sapi
751	17	3.1.170466	60	AC007997	AC007997 Homo sapi	C 824	17	3.1.179681	63	AC013785	AC013785 Homo sapi	824	17	3.1.179681	63	AC013785	AC013785 Homo sapi
752	17	3.1.170571	71	AC031984	AC031984 Homo sapi	C 825	17	3.1.179789	75	AC073349	AC073349 Homo sapi	825	17	3.1.179789	75	AC073349	AC073349 Homo sapi
753	17	3.1.170976	75	AC073981	AC073981 Homo sapi	C 826	17	3.1.180153	65	AC018798	AC018798 Homo sapi	826	17	3.1.180153	65	AC018798	AC018798 Homo sapi
754	17	3.1.171034	82	AP001325	AP001325 Homo sapi	C 827	17	3.1.180570	70	AC026789	AC026789 Homo sapi	827	17	3.1.180570	70	AC026789	AC026789 Homo sapi
755	17	3.1.171200	70	AC025801	AC025801 Homo sapi	C 828	17	3.1.180551	93	HUAC004158	HUAC004158 Homo sapi	828	17	3.1.180551	93	HUAC004158	HUAC004158 Homo sapi
756	17	3.1.171235	76	AC079444	AC079444 Mus muscu	C 829	17	3.1.180791	68	AC023977	AC023977 Homo sapi	829	17	3.1.180791	68	AC023977	AC023977 Homo sapi
757	17	3.1.171436	75	AC074041	AC074041 Mus muscu	C 830	17	3.1.180827	86	AC007344	AC007344 Homo sapi	830	17	3.1.180827	86	AC007344	AC007344 Homo sapi
758	17	3.1.171462	80	AL358052	AL358052 Homo sapi	C 831	17	3.1.181116	68	AC023315	AC023315 Homo sapi	831	17	3.1.181116	68	AC023315	AC023315 Homo sapi
759	17	3.1.171505	83	CNS01DTH	AL132719 Homo sapi	C 832	17	3.1.181121	64	AC016073	AC016073 Homo sapi	832	17	3.1.181121	64	AC016073	AC016073 Homo sapi
760	17	3.1.171592	79	AL160269	AL160269 Homo sapi	C 833	17	3.1.181254	82	AP000825	AP000825 Homo sapi	833	17	3.1.181254	82	AP000825	AP000825 Homo sapi
761	17	3.1.171992	61	AC009266	AC009266 Homo sapi	C 834	17	3.1.181254	82	AP000825	AP000825 Homo sapi	834	17	3.1.181254	82	AP000825	AP000825 Homo sapi
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## ALIGNMENTS

RESULT	1				
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ACCESSION	AB010073	BA000015			
VERSION	AB010073.1	GI:2760169			
SOURCE	Arabidopsis thaliana (strain:Columbia)	DNA, clone:lib:Mtsul P1			
ORGANISM	Arabidopsis thaliana				
REFERENCE	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
AUTHORS	1 (sites)				
TITLE	Sato, S., Kaneko, T., Kotani, H., Nakamura, Y., Asamizu, E., Miyajima, N. and Tabata, S.				
JOURNAL	Structural analysis of Arabidopsis thaliana chromosome 5. IV. Sequence features of the regions of 1,456,315 bp covered by nineteen physically assigned P1 and TAC clones				
MEDLINE	DNA Res. 5 (1), 41-54 (1998)				
REFERENCE	98290546				
AUTHORS	2 (bases 1 to 80376)				
TITLE	Nakamura, Y.				
JOURNAL	Direct Submission				
REFERENCE	Submitted (07-JAN-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research, 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp, Tel: 81-438-52-3935, Fax: 81-438-52-3934)				



**COMMENT**

## FEATURES

**Source**

CDS

CDS

**CDS**

CDS

CDS

CDS

CDS

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Query Match
Best Local Similarity 4.1% Score 23; DB 12; Length 80376;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0:

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Db 62270 TATGTTTCTTATCATATA 62292

RESULT 2
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DEFINITION AC007245
ACCESSION AC007245
VERSION AC007245.3 GI:5649378
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 133137)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
2 (bases 1 to 133137)
McPherson,C., Stromatt,C. and Sapetti,L.
The sequence of Homo sapiens BAC clone RP11-273L18
Unpublished
3 (bases 1 to 133137)
Waterston,R.H.
Direct Submission
Submitted (07-APR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 133137)
Waterston,R.H.
Direct Submission
Submitted (29-JUL-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 133137)
Waterston,R.
Direct Submission

```

```

JOURNAL
COMMENT
Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jul 29, 1999 this sequence version replaced gi:5001515.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0273L18
-----
NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and
sequencing collaboration between the NHGRI Chromosome 7 Mapping
Project (Eric D. Green, director), John D. McPherson in the
Department of Genetics (Washington University), and the Washington
University Genome Sequencing Center. For additional information
about the map position of this sequence, see
http://www.nhgri.nih.gov/DIR/GRB/CHR7, send
mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPc1-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
VECTOR: pBAC3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-121A8, 200 bp overlap.
Actual start of this clone is at base position 130585 of
RP11-121A8; actual end is at 133137 of RP11-273L18.

FEATURES
source
Location/Qualifiers
1..133137
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
/map="7"
/clone="RP11-273L18"
/clone_11b="RPc1-11"
/size="593"
/rpt_family="L1"
849..1105
/rpt_family="L1"
1137..1344
/rpt_family="MIR"
1349..1378
/rpt_family="(TTA)n"
1379..1665
/rpt_family="Alu"
1666..1697
/rpt_family="(TTA)n"
2254..2404
/rpt_family="GA-rich"
4011..4472
/rpt_family="L1"
repeat_region
repeat_region
repeat_region
repeat_region
repeat_region
repeat_region

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repeat_region 4558.4603 /rpt_family="(TG)n"
repeat_region 4706.4789 /rpt_family="MERS3"
repeat_region 5333.5430 /rpt_family="L1"
repeat_region 5681.5976 /rpt_family="L1"
repeat_region 6028.6201 /rpt_family="L1"
repeat_region 6209.6493 /rpt_family="MIR"
repeat_region 6675.7062 /rpt_family="Alu"
misc_feature 7081.7257 /note="match to EST AA703089 (NID:g2706202) z17g11.s1"
repeat_region 7337.7456 /rpt_family="GA-rich"
misc_feature 7477.7520 /note="similar to EST AA076849 (NID:g1836337)"
misc_feature 7743.8105 /note="similar to EST AA310709 (NID:g1963058)"
misc_feature 7963.8105 /note="similar to EST C19100 (NID:g1580702)"
misc_feature 8534.8614 /note="similar to EST AA309744 (NID:g1962093)"
misc_feature 8735.8889 /note="similar to EST AA309744 (NID:g1962093)"
repeat_region 8895.8945 /rpt_family="(TG)n"
repeat_region 8991.9013 /rpt_family="(TTG)n"
repeat_region 9038.9121 /rpt_family="MERS3"
misc_feature 9072.9499 /note="similar to EST T91457 (NID:g723370) ye01g08.r1"
misc_feature 9219.9606 /note="match to EST AA533199 (NID:g2277295) nj11c11.s1"
repeat_region 9653.9748 /rpt_family="L1"
repeat_region 9999.10295 /rpt_family="L1"
repeat_region 10348.10495 /rpt_family="MIR"
repeat_region 10504.10529 /rpt_family="(TTA)n"
repeat_region 10530.10816 /rpt_family="Alu"
repeat_region 10817.10848 /rpt_family="(TTA)n"
repeat_region 11403.11350 /rpt_family="GA-rich"
misc_feature 12131.12514 /note="match to EST A1637495 (NID:g4689729) tt25f01.x1"
repeat_region 13155.13611 /rpt_family="L1"
repeat_region 13612.13638 /rpt_family="(TAA)n"
repeat_region 13704.13747 /rpt_family="(TC)n"
repeat_region 13849.13932 /rpt_family="MERS3"
repeat_region 14463.14560 /rpt_family="L1"
repeat_region 14779.15099 /rpt_family="L1"
repeat_region 15303.15332 /rpt_family="(TTA)n"
repeat_region 15333.15617 /rpt_family="Alu"
repeat_region 15618.15649
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repeat_region 16200.16292 /rpt_family="(TTA)n"
misc_feature 17296.17364 /rpt_family="GA-rich"
misc_feature 17296.17349 /note="similar to EST AA310709 (NID:g1963058)"
repeat_region 17990.18196 /note="similar to EST C19100 (NID:g1580702)"
repeat_region 18197.18499 /rpt_family="L1"
repeat_region 18500.18621 /rpt_family="Alu"
repeat_region 18832.18977 /rpt_family="L1"
repeat_region 18987.19351 /rpt_family="CT-rich"
repeat_region 20180.20500 /rpt_family="L1"
repeat_region 20587.20757 /rpt_family="MIR"
repeat_region 20587.20757 /rpt_family="Alu"

Query Match 4.08; Score 22; DB 86; Length 133137;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 336 AGTATGTTTCTTATCATTA 357
Db 117618 AGTATGTTTCTTATCATTA 117639

RESULT 3
AC023570 151429 bp DNA HTG 20-SEP-2000
LOCUS Homo sapiens chromosome 7 clone RP11-623K16 map 7, WORKING DRAFT
DEFINITION SEQUENCE, 15 unordered pieces.
ACCESSION AC023570
VERSION AC023570.3 GI:10198523
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT;
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 151429)
REFERENCE Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
AUTHORS 2 (bases 1 to 151429)
JOURNAL Homo sapiens chromosome 7, clone RP11-623K16
REFERENCE 2 (bases 1 to 151429)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bede,F., Boguslavsky,L.,
Boukhalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choepeil,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Dearlallan,K., Dewar,K., Dodge,S., Domingo,M., Doyle,M.,
Fenster,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-pierre,N., Grant,G., Hayes,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Landers,T., Largocque,K., Lehoczy,J., Levine,R.,
Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M.,
McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrum,J.,
Meneus,L., Mihova,T., Miranda,C., Mienga,Y., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Olyar,T.M.,
Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C.,
Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Tittell,A.,
Travers,M., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,
Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,D., Zimmer,A. and
Zody,M.
Direct Submission
Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 20, 2000 this sequence version replaced gi:19167819.
```

All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: MIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information -----  
Center project name: L6780  
Center clone name: 623\_K16  
----- Summary Statistics -----  
Sequencing vector: M13; M7815; 100% of reads  
Chemistry: dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 144705 bases at least Q40  
Consensus quality: 147875 bases at least Q30  
Consensus quality: 149247 bases at least Q20  
Insert size: 157000; agarose-fp  
Insert size: 150029; sum-of-contigs  
Quality coverage: 5.0 in Q20 bases; agarose-fp  
Quality coverage: 5.3 in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 15 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved. 8036: contig of 8036 bp in length  
1  
8037 8136: gap of 100 bp  
8137 10849: contig of 2713 bp in length  
10850 10949: gap of 100 bp  
10950 32703: contig of 21754 bp in length  
32704 32803: gap of 100 bp  
32804 37751: contig of 4948 bp in length  
37752 37851: gap of 100 bp  
37852 43829: contig of 5978 bp in length  
43830 43929: gap of 100 bp  
43930 50340: contig of 6411 bp in length  
50341 50440: gap of 100 bp  
50441 55479: contig of 5039 bp in length  
55480 55579: gap of 100 bp  
55580 62760: contig of 7181 bp in length  
62761 62860: gap of 100 bp  
62861 72470: contig of 9610 bp in length  
72471 72570: gap of 100 bp  
72571 83146: contig of 10576 bp in length  
83147 83246: gap of 100 bp  
83247 98629: contig of 15383 bp in length  
98630 98729: gap of 100 bp  
98730 113955: contig of 15226 bp in length  
113956 114055: gap of 100 bp  
114056 128189: contig of 14134 bp in length  
128190 128289: gap of 100 bp  
128290 148106: contig of 19817 bp in length  
148107 148206: gap of 100 bp  
148207 151429: contig of 3223 bp in length.  
Location/Qualifiers  
1. 151429  
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/db\_xref="taxon:9606"  
/chromosome="7"  
/map="7"  
/clone="RP11-623K16"  
/clone\_lib="RP11 Human Male BAC"  
1. 8036  
/note="assembly\_fragment"  
clone\_end:SP6  
vector\_side:left"  
misc\_feature  
8137..10849  
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10950..32703  
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misc\_feature 32804..37751  
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misc\_feature 37852..43829  
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misc\_feature 43930..50340  
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misc\_feature 50441..55479  
/note="assembly\_fragment"  
misc\_feature 55580..62760  
/note="assembly\_fragment"  
misc\_feature 62861..72470  
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misc\_feature 83247..98629  
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misc\_feature 98730..113955  
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misc\_feature 114056..128189  
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misc\_feature 128290..148106  
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misc\_feature 148207..151429  
/note="assembly\_fragment"  
clone\_end:T7  
vector\_side:right"  
BASE COUNT 46908 a 29517 c 28636 g 44907 t 1401 others  
ORIGIN  
Query Match 4.0%; Score 22; DB 68; Length 151429;  
Best local similarity 100.0%; Pred. No. 0.98;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 336 AGTATTGTTTTCATCAATA 357  
|||||  
Db 93038 AGTATTGTTTTCATCAATA 93059  
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RESULT 4  
AC012690/c  
LOCUS Homo sapiens chromosome 10 clone RP11-127B19, WORKING DRAFT  
DEFINITION  
AC012690  
ACCESSION AC012690  
VERSION AC012690.7 GI:10944434  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 172127)  
AUTHORS Smith,D.R.  
TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome  
Sequence Data  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 172127)  
AUTHORS Smith,D.R.  
TITLE Direct Submission  
COMMENT Submitted (03-NOV-1999) Genome Therapeutics Corporation, 100 Beaver  
Street, Waltham, MA 02453, USA  
On Oct 21, 2000 this sequence version replaced gi:6862733.  
----- Genome Center -----  
Center: Genome Therapeutics Corporation  
Center code: GTC  
Web site: <http://www.genomecorp.com/>  
Contact: [gtc-seqcenter@genomecorp.com](mailto:gtc-seqcenter@genomecorp.com)  
----- Project Information -----  
Center project name: hg054  
----- Summary Statistics -----

Sequencing vector: N/A  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 990315  
 Consensus quality: 148903 bases at least Q40  
 Consensus quality: 159968 bases at least Q30  
 Consensus quality: 162621 bases at least Q20  
 Insert size: 170826; sum-of-contrigs  
 Quality coverage: 4.6x in Q20 bases; sum-of-contrigs

NOTE: This is a 'working draft' sequence. It currently consists of 15 contrigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contrigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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* 1 1059: contrig of 1059 bp in length
* 1060 1159: gap of unknown length
* 1160 2591: contrig of 1432 bp in length
* 2592 2691: gap of unknown length
* 2692 3804: contrig of 1113 bp in length
* 3805 3904: gap of unknown length
* 3905 5041: contrig of 1137 bp in length
* 5042 5141: gap of unknown length
* 5142 6813: contrig of 1672 bp in length
* 6814 6913: gap of unknown length
* 6914 8536: contrig of 1623 bp in length
* 8537 8636: gap of unknown length
* 8637 10627: contrig of 1991 bp in length
* 10628 10727: gap of unknown length
* 10728 12325: contrig of 1598 bp in length
* 12326 12425: gap of unknown length
* 12426 14823: contrig of 2398 bp in length
* 14824 14923: gap of unknown length
* 14924 23336: contrig of 8413 bp in length
* 23337 23436: gap of unknown length
* 23437 35598: contrig of 12162 bp in length
* 35599 35698: gap of unknown length
* 35699 54658: contrig of 18960 bp in length
* 54659 54758: gap of unknown length
* 54759 90983: contrig of 36225 bp in length
* 90984 91083: gap of unknown length
* 91084 129108: contrig of 38025 bp in length
* 129109 129208: gap of unknown length
* 129209 172127: contrig of 42919 bp in length.
  
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## FEATURES

## Source

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1. 172127
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/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-127B19"
/clone_1lb="RP11-127B19"
1. 1059
/note="assembly_name:Contig2"
misc_feature
1160. 2591
/note="assembly_name:Contig11"
misc_feature
2692. 3804
/note="assembly_name:Contig19"
misc_feature
3905. 5041
/note="assembly_name:Contig23"
misc_feature
5142. 6813
/note="assembly_name:Contig27"
misc_feature
6914. 8536
/note="assembly_name:Contig28"
misc_feature
8637. 10627
/note="assembly_name:Contig32"
misc_feature
10728. 12325
/note="assembly_name:Contig33"
misc_feature
12426. 14823
/note="assembly_name:Contig34"
misc_feature
14924. 23336
  
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misc_feature /note="assembly_name:Contig35"
23437. 35598
/note="assembly_name:Contig36"
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35699. 54658
/note="assembly_name:Contig37"
misc_feature 54759. 90983
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misc_feature 91084. 129108
/note="assembly_name:Contig39"
misc_feature 129209. 172127
/note="assembly_name:Contig40"
BASE COUNT 48733 a 37356 c 37151 g 47466 t 1421 others
ORIGIN
  
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Query Match 4.0%; Score 22; DB 63; Length 172127;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 324 TTTCCTAGTCACGATGTTT 345
|||||
Db 31919 TTTCCTAGTCACGATGTTT 31898
  
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RESULT 5
HSATP7A06 348 bp DNA PRI 04-APR-1996
LOCUS Human Menkes disease gene (ATP7A), exon 6.
DEFINITION U27365
ACCESSION U27365.1 GI:987236
VERSION 6 of 23
KEYWORDS human.
SEGMENT 6 of 23
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 348)
AUTHORS Dierick,H.A., Ambrosini,L., Spencer,J., Glover,T.W. and Mercer,J.F.
TITLE Molecular structure of the Menkes disease gene (ATP7A)
JOURNAL Genomics 28 (3), 462-469 (1995)
MEDLINE 96039257
REFERENCE 2 (bases 1 to 348)
AUTHORS Dierick,H.A.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-1995) H.A. Dierick, Pediatrics, University of
Michigan, 1301 East Catherine, Ann Arbor, MI 49109-0618, USA
  
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## FEATURES

## Source

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1. 348
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="Xq13"
/chromosome="X"
96. 259
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/number=6
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/organism="ATP7A"
/note="exon not sequenced completely; this part of
sequence from Genbank Accession Number L06133"
BASE COUNT 114 a 46 c 73 g 115 t
ORIGIN
  
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Query Match 3.6%; Score 20; DB 92; Length 348;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 337 GTATTGTTTCTATCAAT 356
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Db 68 GTATTGTTTCTATCAAT 87
  
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/protein_id="AAA83285.1"
/db_xref="GI:1118047"
/translation="MDENRMKRLMEEMFTYSICQAMWGLDKENYKKKEIRSLRISVNR
YSSPOLCCSLPTSLIRLSAOCIOKIIIEVPAVVKVPRSKAFLEFVSNFSSSLAF
VIDPSNTRNFCVENNYKEITMTSYETPEFPIIDMMNOVSLKMKRSECMNFV
CIDERNYTKHYKTFGLLPKRETRRLSNGRELLTFKQPTTLTISIDSSNDDSDDE
KIDSNNAEREELLIVENELKRONNETTSSRECSOCPCTSNPKKRNKO"
gene
CDS
complement(join(9858..10065,10400..10629,10709..10880,
10958..11034))
/gene="R04A9.4"
complement(join(9858..11034))
/gene="R04A9.4"
/note="coded for by C. elegans cDNA yk74a6.3: Similar to
eukaryotic initiation factor 4E (Eif-4E)."
/codon_start=1
/protein_id="AAA83286.1"
/db_xref="GI:1118048"
/translation="MSEFPVAPAGTISHPVYKLRMTWYVYVNDERKNSMEETLRNV
TSSVGEFMAHDSIKPPSGLNPSDYNTFRDGIETPMMEVPOQNGRMLITTEKRT
PEIMDTWEILMAMIGEOFSDIESLGIICVNRGRKSKISVTWNSADGKANLIG
GVLKQVYLNNAASMIHORPLVDVLRTEDEHSCOKTSSGVAKAHYAVREERKAPV
STETPATPAT"
complement(12853..22868)
/gene="R04A9.5"
complement(join(12853..12939,13613..13857,15045..15159,
15216..15568,15771..15863,16101..16266,18168..18263,
18536..18592,18675..18758,18811..18879,20854..21723,
22761..22868))
/gene="R04A9.5"
/note="similar to homeobox proteins and to human
centromeric protein E (SP:CEME_HUMAN,002224) and to
ribosomal protein S6 kinase"
/codon_start=1
/evidence="not experimental"
/protein_id="AAA83287.1"
/db_xref="GI:1118049"
/translation="MKQVSMQKFEKLFYDDVAPKPFERKLKLVGEGCKRQVOROKT
GDKGTIVAMKVITKRVKVTGDEKDLHARDERKILETINSPLCDLHVAFQTEKLYL
VLEFGLGELVTLERKSDMPEYARFYSELIIATEHLGHDIYVRDLKPDVNMKLT
AGHVVLTDGLCKYKLRKGEKTLFCGTHEYAPEMIRKRGVGHADVAVLGLTMD
FKGGPFGTETPADKDKSLIKGKVRLPKLSAGKLRIRIIRKDPILRTIPDIKEH
EPEEETDMKIMAHDEPPREKPTLANLEVDSEFTSIAPESCKAITTYTHYLE
LILFLRSMSPENGRILNKNKNSKAPVNLNKSMDVLTBEELTKTNGVLAHLRLS
NVKRYKRLDENVDYIEVQKGFMYLLSIGROENKIQTPSMKPFQCSIDLKDDTT
DEDCMSLGSVLEFRPDSLSPIKIKICPGPKATVGGRAEGAVHGFMSRYKTHLY
TKLIMGSIIPSNKRIMSESOVRLNASEFARNCHPTAIGMOKLSERCGIRYKTIIDN
FTIRKDKICEETNACCRIREPLISREDDTYSIETNEVOTVLEDELEIHLISKR
FTLGYHYIMEKTDLPASYIRAOYEMMRKLSKIDGSKNIGDSEGLNKRYKAKNK
GYRORERIKAKGLSERQVRYNFKRKRTTERKLVKADPKDFTLTKOTVDEMKIA
ERRRKPNDYIIOIANRLGVSHITLCSFIDMOKSIYAGKAK"
33227..33687
/gene="R04A9.1"
join(33227..33337,33487..33687)
/gene="R04A9.1"
/codon_start=1
/evidence="not experimental"
/protein_id="AAA83288.1"
/db_xref="GI:1118050"
/translation="MKLTPEPSFLFKPPASHMLVKESHLYVAMFLRILLITVITV
NSNAMYVPSERKVSITDFCSFRVPCAPGHLCHEGFCIOQOQSSSPRRMYPSLRR
R"
38740..38811
/note="Gin; codon recognized: CAA"
BASE COUNT 16840 a 9604 c 9313 g 17189 t
ORIGIN
Query Match 3.6%; Score 20; DB 5; Length 52946;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 338 TATTGTTTCTATCATATA 357
|||||

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Db 27384 TATTGTTTCTATCATATA 27403
RESULT 8
HS465G10B/C
LOCUS
DEFINITION
HS465G10B 74432 bp DNA PRI 23-NOV-1999
Human DNA sequence from PAC 465G10 on chromosome X contains Menkes
Disease (ATP7A) putative Cu++-transporting P-type ATPase exons 2 to
21, PGAM-B, ESTs.
ACCESSION
294801
VERSION
294801.1 GI:2052037
KEYWORDS
ATP7A; Cu++-transporting ATPase; Menkes Disease; P-type ATPase;
PGAM-B; X.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 74432)
AUTHORS
Bird,C.
TITLE
Direct Submission
JOURNAL
Submitted (23-APR-1997) E-mail enquiries: humquery@sanger.ac.uk
COMMENT
Clone requests: clonerequest@sanger.ac.uk
IMPORTANT: This sequence is not the entire insert of clone 465G10.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The true right end of clone 465G10 is at 74432.
The sequence from clone 465G10 has been finished in more than one
contig. This sequence (465G10B) is separated from the preceding one
(HS465G10A 294753) by a gap of 500 bp sized by PCR and restriction
analysis. 465G10 is from the library RPc3 constructed at the
Roswell Park Cancer Institute by the group of Pieter de Jong. For
further details see http://bacpac.med.buffalo.edu/VECTOR:pcpPAC2.
location/Qualifiers
1. 74432
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/map="X"
/clone="RP3-465G10"
/clone_1b="RPc1-3"
3. 186
/note="AluX repeat: matches 117..300 of consensus;
incomplete repeat"
complement(join(402..526,1055..1258,3110..3252,4861..5007,
10022..10238,12261..12443,14400..14594,22765..22899,
23446..23600,27963..28090,29091..29182,30732..30965,
32170..32395,32592..32668,34381..34742,40608..40771,
45160..45366,53887..54613,55115..55604,72084..72203))
/note="similar to L06133"
/codon_start=1
/product="Menkes Disease (ATP7A)"
/protein_id="CA808162.2"
/db_xref="GI:5262841"
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/translation="MDPSMGVNSVTSIVSGMTCNSCWITIEQIGKVGNGVHHIKVSL
EKNAITIDPKLOTPELOADMDGFDAVIRHDPDLPVLTDTLFLTVASLTLPMDH
IOSTLTKTGVDIKIYPOKRYAVVILIPISIVANOIKELVPELSIDTGLKSGAC
EDHSMOAGEVYIKMVEGMCSTSTIEGKIQGQORIKVSIIDNOEARTIVYQPH
LISVEERKQIEMGFPAYRKQPKTLKAGADVERKNTPVKSSGSSQSSSTYND
STAFITIIDMHCKSVSNIESTLSAQVYSIVLSLNSAIVKYVASSVTPESLKRKA
IEAVSPGLYRVSITSEVSTSNSSSLOKIPLVNVSOPLOQETVINIDGMTCNSCV
OSIEGIVISKRPVKSIRVLSANGNVEYEDPLTSETLGALEIDMGFPATYSGTNEP
LVYIAOPEMPLLTSTNEFYTGMPVODKEGKSSCYIOVGTMCASVANTER
NLRRERGIYSIIYALMACKAERYNNAVIOPPRIAFIRIELCGATVIEADBGQVY
ELVYRGMTCAVCYAKTESITKRGILYSVALATKAKHAKITDPEITGPDITITIEG
LGEASLVAKDRSASHLDHKRETRORRSFVLSLFCIPVMGLMITYMWDDHIFATLH

```

HNQNMSEKEMINLHSSMFLERQILPEGLSYMNLISFLCVPVFGGWFFYIOAYKALK  
 HRTANMDVLIVATTIAFAYSLIILLVAMYERAKVNPITEFPTPMLPEFIALGRLE  
 HIAKGTSEALAKLILSLQATEIVTLDSNDILREQVDIVLQGDILKVPGGKE  
 PVDGRIEBSHWDESILGTGEMPAKKGSTVIGSIQNSGLICAHVADTTIS  
 QVAKLVEAOTSAPILQOFADKLSGFVFFVFSATILNVIIGLNFELVEYFER  
 GYNREISRETEILIRAFQASTIVLCIACCSGLATPRAWGTGCGAQNGLIKGE  
 PLEMAHKVAVFDKTTGTTTGTPTVAVNQKVLIFESRNISSHNLAIIVGAESENHPL  
 GAITRYCKQELDTFTLGTCLDFOVAPGCGISCKVNIENGLLHKNNMNIEDNNIKNAS  
 LVQIDASNEQSTSSSMITDAQISSALNNOQKVLIGNENWIRNGLYINNDVDFMT  
 EHERKGRATVAVAGDELGLAIADTVPEAEALAIHLKSGLEIVLMTGDSKTAR  
 STASOVGIVKVAEVLPSHKVAKROLOEGEKRVAMGGIDSPALMANANYGIAIGT  
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 1708. .2008  
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 2270. .2571  
 /note="AlusP repeat: matches 1. .303 of consensus"  
 3879. .3958  
 /note="L1ME3 repeat: matches 437. .516 of consensus"  
 4211. .4513  
 /note="AlusQ repeat: matches 1. .303 of consensus"  
 5838. .5863  
 /note="L13 copies of 2 mer 100 % conserved"  
 6373. .6576  
 /note="MER3 repeat: matches 5. .209 of consensus"  
 7052. .7243  
 /note="AlusQ repeat: matches 194. .3 of consensus;  
 incomplete repeat"  
 repeat\_region  
 /note="MIR2 repeat: matches 17. .142 of consensus"  
 8805. .9101  
 /note="AlusX repeat: matches 5. .301 of consensus"  
 9389. .9454  
 /note="2 copies of 33 mer 91 % conserved"  
 10448. .10741  
 /note="AlusQ repeat: matches 1. .300 of consensus"  
 11141. .11418  
 /note="L1MA2 repeat: matches 12. .311 of consensus"  
 11765. .11867  
 /note="L1MB6 repeat: matches 809. .912 of consensus"  
 11806. .11883  
 /note="L1MA10 repeat: matches 996. .1069 of consensus"  
 12855. .13154  
 /note="AlusX repeat: matches 1. .301 of consensus"  
 13156. .13328  
 /note="MER42B repeat: matches 1025. .1204 of consensus"  
 13210. .13350  
 /note="MER42C repeat: matches 1183. .1325 of consensus"  
 13217. .13407  
 /note="L1MC3 repeat: matches 2278. .2452 of consensus"  
 13409. .13700  
 /note="AlusQ repeat: matches 295. .2 of consensus"  
 15220. .15353  
 /note="AlusB repeat: matches 14. .142 of consensus;  
 incomplete repeat"  
 repeat\_region  
 /note="AlusQ repeat: matches 1. .299 of consensus"  
 15656. .15824  
 /note="AlusD repeat: matches 134. .302 of consensus;  
 incomplete repeat"  
 repeat\_region  
 /note="L1 repeat: matches 4904. .4191 of consensus"  
 16679. .16978  
 /note="AlusQ repeat: matches 299. .1 of consensus"  
 16983. .18272  
 /note="L1 repeat: matches 2906. .1620 of consensus"  
 18298. .18545  
 /note="MER25 repeat: matches 1806. .1526 of consensus"  
 19460. .20291

/note="L1 repeat: matches 4546. .5390 of consensus"  
 20148. .21015  
 /note="L1PA16 repeat: matches 1. .865 of consensus"  
 21028. .21327  
 /note="AlusX repeat: matches 1. .300 of consensus"  
 21350. .21388  
 /note="L1PA15 repeat: matches 859. .897 of consensus"  
 21413. .21488  
 /note="FRAM repeat: matches 158. .83 of consensus"  
 22102. .22207  
 /note="MER repeat: matches 174. .63 of consensus"  
 22271. .22465  
 /note="MIR repeat: matches 262. .56 of consensus"  
 23025. .23332  
 /note="AlusD repeat: matches 1. .300 of consensus"  
 23931. .24072  
 /note="MER20 repeat: matches 80. .214 of consensus"  
 24086. .24379  
 /note="AlusB repeat: matches 5. .302 of consensus"  
 24755. .25136  
 /note="THE1C repeat: matches 1. .368 of consensus"  
 25149. .25313  
 /note="THE1B-INTERNAL repeat: matches 1. .164 of consensus"  
 25321. .25622  
 /note="AlusP repeat: matches 303. .1 of consensus"  
 25623. .25768  
 /note="THE1B-INTERNAL repeat: matches 150. .295 of  
 consensus"  
 25770. .26070  
 /note="Alus repeat: matches 1. .301 of consensus"  
 26086. .26238  
 /note="THE1B-INTERNAL repeat: matches 279. .430 of  
 consensus"  
 26277. .27437  
 /note="THE1B-INTERNAL repeat: matches 427. .1580 of  
 consensus"  
 27438. .27794  
 /note="THE1C repeat: matches 1. .369 of consensus"  
 29421. .29719  
 /note="AlusQ repeat: matches 300. .1 of consensus"  
 29759. .29947  
 /note="L1MB4 repeat: matches 12. .208 of consensus"  
 31239. .31365  
 /note="FLAM\_A repeat: matches 133. .5 of consensus"  
 31720. .31901  
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 33493. .33710  
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 33938. .34168  
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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 337 GATTGTTTCTTATCAAT 356  
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 Db 40800 GATTGTTTCTTATCAAT 40781  
 RESULT 9  
 AP001089/c AP001089 87022 bp DNA HTG 30-MAY-2000  
 LOCUS Homo sapiens chromosome 18 clone RP11-693M17 map 18p11.3, WORKING  
 DEFINITION





```

OY      328      CTAGTCTCAGTATGTTTTT      347
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Db      27343      CTAGTCTCAGTATGTTTTT      27324

RESULT  10
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LOCUS      AC006778
DEFINITION      Caenorhabditis elegans clone Y47C4, *** SEQUENCING IN PROGRESS ***
ACCESSION      AC006778
VERSION      AC006778.3
KEYWORDS      HTG; HTGS_PHASE1
SOURCE      Caenorhabditis elegans.
ORGANISM      Caenorhabditis elegans.
REFERENCE      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
AUTHORS      Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
TITLE      1 (bases 1 to 132749)
JOURNAL      Waterston, R.H.
REFERENCE      The sequence of Caenorhabditis elegans clone
AUTHORS      Unpublished
TITLE      2 (bases 1 to 132749)
JOURNAL      Waterston, R.H.
REFERENCE      Direct Submission
AUTHORS      Submitted (23-FEB-1999) Genome Sequencing Center, Washington
TITLE      University School of Medicine, 4444 Forest Park Parkway, St. Louis
JOURNAL      MO 63108, USA

COMMENT  * NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1
* 2081      2080: contig of 2080 bp in length
* 2095      2094: gap of unknown length
* 4242      4242: contig of 2148 bp in length
* 4243      4256: gap of unknown length
* 4257      13398: contig of 9142 bp in length
* 13399      13412: gap of unknown length
* 13413      132749: contig of 119337 bp in length.
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* Location/Qualifiers
* 1..132749
* /organism="Caenorhabditis elegans"
* /db_xref="taxon:6239"
* /clone="Y47C4"

BASE COUNT      42651 a      22976 c      23008 g      44072 t      42 others
ORIGIN

Query Match      3.6%      Score 20;      DB 60;      Length 132749;
Best Local Similarity 100.0%;      Pred. No. 11;
Matches 20;      Conservative 0;      Mismatches 0;      Indels 0;      Gaps 0;

OY      338      TATTGTTTTCTTATCAATA      357
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Db      128941      TATTGTTTTCTTATCAATA      128960

RESULT  11
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LOCUS      AC036162
DEFINITION      Homo sapiens chromosome 17 clone RP11-143J12 map 17, WORKING DRAFT
ACCESSION      AC036162
VERSION      AC036162.2
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.  
1 (bases 1 to 142362)  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens chromosome 17, clone RP11-143J12  
Unpublished  
2 (bases 1 to 142362)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Baldwin, J., Barua, N., Bastien, V., Beda, F.,  
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,  
Campolino, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,  
Collymore, A., Cooke, P., DeArnell, K., Dewar, K., Diaz, J. S.,  
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,  
Galagan, J., Gaidyna, S., Ginde, S., Goyette, M., Graham, L.,  
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
Holland, J. C., Iliev, I., Johnson, R., Jones, C., Kamp, L., Karlas, A.,  
Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lechoczy, J.,  
Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N.,  
McCarthy, J. M., McEwan, P., McGuirk, A., McKernan, K., McPheters, R.,  
Meldrum, J., Meneses, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,  
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,  
O'Neill, D., Olyar, T. M., Oliver, J., Peterson, K., Pierre, N.,  
Plisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rotman, D.,  
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Testa, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,  
Vassiliadis, H., Viel, R., Vo, A., Wilson, G., Wu, X., Wyman, D., Ye, W. J.,  
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (07-APR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On May 14, 2000 this sequence version replaced g1:75238350.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: MIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information  
Center project name: L9139  
Center clone name: 143.J12

Summary Statistics  
Sequencing vector: M13: M77815; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 129334 bases at least Q40  
Consensus quality: 136360 bases at least Q30  
Consensus quality: 138873 bases at least Q20  
Insert size: 151000; agarose-fp  
Insert size: 140262; sum-of-contigs  
Quality coverage: 3.7 in Q20 bases; agarose-fp  
Quality coverage: 4.0 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently  
\* consists of 22 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1203: contig of 1203 bp in length  
\* 1204 1303: gap of 100 bp  
\* 1304 2675: contig of 1372 bp in length  
\* 2676 2775: gap of 100 bp  
\* 2776 4179: contig of 1404 bp in length  
\* 4180 4279: gap of 100 bp  
\* 4280 6165: contig of 1886 bp in length  
\* 6166 6265: gap of 100 bp  
\* 6266 8694: contig of 2429 bp in length  
\* 8695 8794: gap of 100 bp  
\* 8795 12147: contig of 3353 bp in length

clone\_end:SP6

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 6 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 9265: contig of 9265 bp in length  
 \* 9266 9365: gap of unknown length  
 \* 9366 26504: contig of 17139 bp in length  
 \* 26505 26604: gap of unknown length  
 \* 26605 44300: contig of 17696 bp in length  
 \* 44301 44400: gap of unknown length  
 \* 44401 62250: contig of 17850 bp in length  
 \* 62251 62350: gap of unknown length  
 \* 62351 105744: contig of 43394 bp in length  
 \* 105745 105844: gap of unknown length  
 \* 105845 155172: contig of 49328 bp in length.

FEATURES  
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 /chromosome="18"  
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 /note="assembly\_name:Contig2"  
 misc\_feature 26605. .44300  
 /note="assembly\_name:Contig3"  
 clone\_end:47  
 vector\_side:right"  
 44401. .62250  
 /note="assembly\_name:Contig4"  
 misc\_feature 62351. .105744  
 /note="assembly\_name:Contig5"  
 misc\_feature 105845. .155172  
 /note="assembly\_name:Contig6"  
 BASE COUNT 51543 a 28385 c 28043 g 46698 t 503 others  
 ORIGIN

Query Match 3.6% Score 20; DB 66; Length 155172;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 TAGTGTGTTAAGAACTT 228  
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 Db 35799 TACTGTGTTAAGAACTT 35780

RESULT 13  
 AC011921  
 LOCUS Homo sapiens chromosome 17 clone RP11-15E18 map 17, WORKING DRAFT  
 DEFINITION  
 AC011921  
 AC011921.5 GI:12043897  
 VERSION HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 155261)  
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
 Homo sapiens chromosome 17, clone RP11-15E18  
 JOURNAL  
 TITLE  
 REFERENCE  
 AUTHORS  
 2 (bases 1 to 155261)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,  
 Baldwin,J., Barna,N., Beckerly,R., Bonuslavsky,L., Boukhgalter,B.,  
 Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,  
 Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,  
 Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,

# TITLE JOURNAL COMMENT

Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
 Howland,J.C., Johnson,R., Jones,C., Kann,L., Karats,A., Klein,J.,  
 Lehoczy,J., Lien,C., Locke,K., McDonald,P., Marquis,N.,  
 McKean,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,  
 Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
 Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,  
 Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (16-OCT-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Jan 7, 2001 this sequence version replaced g1:9369474.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu

Project Information  
 Center project name: L3450  
 Center clone name: 15\_E\_18

Summary Statistics  
 Sequencing vector: M13; M7815; 35% of reads  
 Sequencing vector: Plasmid; n/a; 65% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960721  
 Consensus quality: 152128 bases at least Q40  
 Consensus quality: 152881 bases at least Q30  
 Consensus quality: 153204 bases at least Q20  
 Insert size: 153000; agarose-1p  
 Insert size: 154561; sum-of-coverage

Quality coverage: 13.7 in Q20 bases; agarose-1p  
 Quality coverage: 13.5 in Q20.  
 NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 8 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 64950: contig of 64950 bp in length  
 \* 64951 65050: gap of 100 bp  
 \* 65051 66096: contig of 1046 bp in length  
 \* 66097 66196: gap of 100 bp  
 \* 66197 68004: contig of 1808 bp in length  
 \* 68005 68104: gap of 100 bp  
 \* 68105 72490: contig of 4386 bp in length  
 \* 72491 72590: gap of 100 bp  
 \* 72591 91407: contig of 18817 bp in length  
 \* 91408 91507: gap of 100 bp  
 \* 91508 109552: contig of 18045 bp in length  
 \* 109553 109652: gap of 100 bp  
 \* 109653 147065: contig of 37413 bp in length  
 \* 147066 147165: gap of 100 bp  
 \* 147166 155261: contig of 8096 bp in length.

FEATURES  
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BASE COUNT 46003 a 32520 c 32733 g 43304 t 701 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 100 TGGTTAATATATGAGATAA 119
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Db 136610 TGGTTAATATGAGATAA 136629

RESULT 14
AL161417 159999 bp DNA HTG 07-FEB-2001
LOCUS Homo sapiens chromosome 13 clone RP11-125A7, ** SEQUENCING IN
DEFINITION
ACCESSION AL161417
VERSION AL161417.15 GI:12717956
KEYWORDS HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 159999)
Dunn,M.
Direct Submission
Submitted (06-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Feb 8, 2001 this sequence version replaced gi:11266228.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: ba125A7
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 159245 bases at least Q40
Consensus quality: 159657 bases at least Q30
Consensus quality: 159801 bases at least Q20
Insert size: 159899; sum-of-contigs
Insert size: 146490; 14.2% error; agarose-fp
Quality coverage: 8.64x in Q20 bases; sum-of-contigs Quality
coverage: 10.73x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 157307: contig of 157307 bp in length
* 157308 157407: gap of 100 bp
* 157408 159999: contig of 2592 bp in length.
Location/Qualifiers
FEATURES
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            /note="assembly_fragment:00188
            clone_end:SP6
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            157408..159999
            /note="assembly_fragment:04213"
BASE COUNT 52184 a 29004 c 28902 g 49809 t 100 others
ORIGIN

Query Match 3.6%; Score 20; DB 79; Length 159999;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 143 CTGTTAAAGCAGTGTGCT 162
    |||||||||||||||||||
Db 103976 CTGTTAAAGCAGTGTGCT 103995

RESULT 15
AC025515 164746 bp DNA HTG 03-APR-2000
LOCUS AC025515/C
DEFINITION Homo sapiens chromosome 17 clone RP11-634F5 map 17, WORKING DRAFT
SEQUENCE 29 unordered pieces.
ACCESSION AC025515.2 GI:7387415
VERSION AC025515.2 GI:7387415
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 164746)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 164746)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choquel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Glade,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heathford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karlas,A.,
Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Liu,G., Liu,G., Locke,K., Macdonald,P., Marguier,S.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrum,J., Menus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talmas,J.,
Tessaye,S., Theodores,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (09-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 3, 2000 this sequence version replaced gi:7212099.
All repeats were identified using RepeatMasker:
Smt, A.F.A. & Green, P. (1996-1997)
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BASE COUNT      44713 a 34820 c 34127 g 48284 t 2802 others
ORIGIN

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Query Match      3.6%; Score 20; DB 69; Length 164746;
Best Local Similarity 100.0%; Pred. NO. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 100 TGGTTAATATATGGAATTA 119
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Db 120129 TGGTTAATATATGGAATTA 120110

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Search completed: May 31, 2001, 01:50:24  
 Job time: 6831 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2001, 01:02:39 ; Search time 115.37 Seconds  
(without alignments)  
2808.344 Million cell updates/sec

Title: US-09-382-242-23

Perfect score: 555  
Sequence: 1 ATGCTTTAAACAAGCACTC.....AATCATACACTTAACGATAG 555

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapept 60.0

Searched: 678276 seqs, 291890651 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	100.0	555	18	T79321 DNA encoding Staph
2	21	3.8	31	18	T79300 Staphylothermus ma
3	21	3.8	52	18	T79299 Staphylothermus ma
4	18	3.2	25002	19	V52181 Streptococcus pneu
5	18	3.2	29604	18	X83005 Human secreted pro
6	17	3.1	157	20	X52014 Human secreted pro
7	17	3.1	209	21	A41434 Human secreted exp
8	17	3.1	361	21	C03852 Human secreted pro
9	17	3.1	422	16	T26471 Human gene signatu
10	17	3.1	486	21	C35823 Zea mays DNA fragm
11	17	3.1	498	21	C94715 Cat flea hindgut a

C	12	17	3.1	849	20	Z16638 Human gene express
C	13	17	3.1	909	21	C74317 Human secreted pro
C	14	17	3.1	1121	11	O06623 Asparagine synthet
C	15	17	3.1	1563	21	A99072 Arabidopsis thalia
C	16	17	3.1	1660	18	T94661 Chrysanthemum flav
C	17	17	3.1	1829	20	X84982 Human secreted pro
C	18	16	2.9	191	16	T21422 Human gene signatu
C	19	16	2.9	269	21	C31195 Human secreted pro
C	20	16	2.9	333	20	X05168 Human MSH5 (hMSH5)
C	21	16	2.9	333	21	A43208 Xenopus secreted e
C	22	16	2.9	482	21	C38143 Zea mays DNA fragm
C	23	16	2.9	500	21	C94177 Cat flea head and
C	24	16	2.9	542	18	T80087 Fragment #2 of the
C	25	16	2.9	593	21	A16400 Human colon cancer
C	26	16	2.9	715	20	Z15052 Human gene express
C	27	16	2.9	830	21	C59909 Human secreted pro
C	28	16	2.9	837	21	A38000 H. influenzae dime
C	29	16	2.9	988	21	A02629 Human colon cancer
C	30	16	2.9	1067	20	X13670 Enterococcus faeca
C	31	16	2.9	1120	20	X13658 Enterococcus faeca
C	32	16	2.9	1171	20	X61401 DNA encoding a hum
C	33	16	2.9	1221	21	Z33340 Human secreted pro
C	34	16	2.9	1330	14	O40567 Mouse IL-1. Mus m
C	35	16	2.9	1339	21	A99191 Mouse interleukin-
C	36	16	2.9	1488	20	C06653 hkv5.1 human brain
C	37	16	2.9	1520	21	C64786 Lemon acyl transfe
C	38	16	2.9	1520	21	C34501 Arabidopsis thalia
C	39	16	2.9	1623	21	C74351 Human secreted pro
C	40	16	2.9	1668	20	Z27257 Human secreted pro
C	41	16	2.9	1688	21	C39339 Arabidopsis thalia
C	42	16	2.9	1670	21	C51452 Arabidopsis thalia
C	43	16	2.9	1700	19	V11858 Mus musculus Tub I
C	44	16	2.9	1756	19	X14238 Arabidopsis thalia
C	45	16	2.9	1769	21	C51449 Arabidopsis thalia
C	46	16	2.9	1777	21	C42051 Arabidopsis thalia
C	47	16	2.9	1850	21	C52840 Arabidopsis thalia
C	48	16	2.9	1880	20	Z06652 Arabidopsis thalia
C	49	16	2.9	2455	21	F22468 Human secreted pro
C	50	16	2.9	2483	17	T12462 Human K+ channel 2
C	51	16	2.9	2483	19	V04874 H. pylori cellula
C	52	16	2.9	2751	19	X30434 Arabidopsis thalia
C	53	16	2.9	2784	18	T68270 Arabidopsis thalia
C	54	16	2.9	3383	19	V21160 Arabidopsis thalia
C	55	16	2.9	3386	18	T60656 Arabidopsis thalia
C	56	16	2.9	3386	20	X23865 Arabidopsis thalia
C	60	16	2.9	3386	20	V81164 Arabidopsis thalia
C	61	16	2.9	3386	21	A96581 Arabidopsis thalia
C	62	16	2.9	3386	21	Z44013 Arabidopsis thalia
C	63	16	2.9	3386	22	C90224 Arabidopsis thalia
C	64	16	2.9	3386	22	C90224 Arabidopsis thalia
C	65	16	2.9	4051	21	A37997 H. influenzae dmsa
C	66	16	2.9	4674	20	X90421 Human ataxin-2 lik
C	67	16	2.9	7100	21	A99202 Mouse interleukin-
C	68	16	2.9	8278	22	C89138 Canine retrovirus
C	69	16	2.9	8805	20	X13072 Enterococcus faeca
C	70	16	2.9	8892	16	O94266 Osteoinductive ret
C	71	16	2.9	20383	21	E93709 F-box protein Cdc4
C	72	16	2.9	30115	20	A59651 Modified adenovira
C	73	16	2.9	32768	20	X13336 Enterococcus faeca
C	74	16	2.9	35515	20	X20252 Borrelia burgdorfe
C	75	16	2.9	38258	19	V17876 Cloned toxin gene
C	76	16	2.9	38258	20	Z23895 Murine LOBO homo
C	77	16	2.9	103929	21	F22287 Arabidopsis thalia
C	78	16	2.9	611590	20	X20248 Borrelia burgdorfe
C	79	16	2.9	910715	21	F22303 Borrelia burgdorfe
C	80	16	2.9	1664976	19	V21209 Methanococcus jan
C	81	15	2.7	122	16	T05586 Human islet p69 cd
C	82	15	2.7	138	21	C20546 Human secreted pro
C	83	15	2.7	173	21	Z00371 Partial nucleotide
C	84	15	2.7	184	21	C12531 Human secreted pro

C 85	15	2.7	209	21	C24754	Human secreted pro
C 86	15	2.7	234	21	A66120	E. coli proliferat
C 87	15	2.7	237	21	A65871	E. coli proliferat
C 88	15	2.7	243	21	A41556	Human secreted exp
C 89	15	2.7	244	21	C09203	Human secreted pro
C 90	15	2.7	257	20	X34844	Differentially exp
C 91	15	2.7	261	21	A65991	E. coli proliferat
C 92	15	2.7	269	21	A40748	Wild type human CD
C 93	15	2.7	276	20	V89047	EST clone BV93. H
C 94	15	2.7	295	21	C28640	Human secreted pro
C 95	15	2.7	300	20	Z14193	Human gene express
C 96	15	2.7	313	18	V78666	Staphylococcus aur
C 97	15	2.7	331	21	C06504	Human secreted pro
C 98	15	2.7	348	21	F21039	Human secreted pro
C 99	15	2.7	348	21	A34917	Human low adenosin
C 100	15	2.7	353	21	C09227	Human adenosine re
C 101	15	2.7	377	21	C53208	Human secreted pro
C 102	15	2.7	388	21	C03515	Arabidopsis thalia
C 103	15	2.7	429	21	A79675	Human secreted pro
C 104	15	2.7	472	18	V75044	Eucalyptus grandis
C 105	15	2.7	476	21	C16919	Staphylococcus aur
C 106	15	2.7	486	19	T98788	Human secreted pro
C 107	15	2.7	495	21	X61626	DNA encoding two S
C 108	15	2.7	546	20	X61625	B. burgdorferi ant
C 109	15	2.7	567	20	X13601	B. burgdorferi ant
C 110	15	2.7	614	21	C33864	Enterococcus faeca
C 111	15	2.7	631	21	X20952	Arabidopsis thalia
C 112	15	2.7	671	21	F13337	Polynucleotide seq
C 113	15	2.7	685	20	Z42095	Aspergillus oryzae
C 114	15	2.7	687	20	X13549	Human endometrium
C 115	15	2.7	716	12	Q10059	Enterococcus faeca
C 116	15	2.7	717	12	C16339	Ovine FSH alpha su
C 117	15	2.7	771	21	C79351	Human ORFX ORF1894
C 118	15	2.7	800	20	Z20370	Plant viral move
C 119	15	2.7	821	21	X13673	Gene encoding bact
C 120	15	2.7	821	21	C98850	Enterococcus faeca
C 121	15	2.7	901	21	X55619	Human pancreatic c
C 122	15	2.7	901	21	C46900	Sequence of mouse
C 123	15	2.7	903	21	C43172	Arabidopsis thalia
C 124	15	2.7	965	20	X13459	Arabidopsis thalia
C 125	15	2.7	977	21	C36434	Enterococcus faeca
C 126	15	2.7	1011	20	Z41348	Arabidopsis thalia
C 127	15	2.7	1016	17	T48041	Human normal uteru
C 128	15	2.7	1065	21	Z60356	Yeast chromosome I
C 129	15	2.7	1086	21	C46471	DNA encoding a 36
C 130	15	2.7	1184	21	C46473	Arabidopsis thalia
C 131	15	2.7	1192	21	F22356	Arabidopsis thalia
C 132	15	2.7	1200	21	F16053	Human secreted pro
C 133	15	2.7	1203	20	Z08866	Human prostate can
C 134	15	2.7	1203	20	X17787	Mouse interleukin-
C 135	15	2.7	1203	21	A52578	Mouse interleukin-
C 136	15	2.7	1216	16	O87295	Murine interleukin
C 137	15	2.7	1216	21	F13529	Rat regucalcin cDN
C 138	15	2.7	1290	21	C42067	Aspergillus oryzae
C 139	15	2.7	1306	13	C27827	Arabidopsis thalia
C 140	15	2.7	1338	20	X61518	Bovine TP (CDNA cl
C 141	15	2.7	1341	13	Q27559	B. burgdorferi ant
C 142	15	2.7	1353	21	Z39862	Human para-influen
C 143	15	2.7	1363	20	X55620	Plasmodium ovale P
C 144	15	2.7	1374	15	Q72874	Sequence of mouse
C 145	15	2.7	1405	19	V59550	Phosphatase Dbpa.
C 146	15	2.7	1410	20	X61517	Human secreted pro
C 147	15	2.7	1419	20	X22716	B. burgdorferi ant
C 148	15	2.7	1473	16	O87715	Human cytochrome P
C 149	15	2.7	1473	17	T28381	Human cytochrome P
C 150	15	2.7	1473	17	T17404	Human cytochrome P
C 151	15	2.7	1475	21	C36317	Human derived cyto
C 152	15	2.7	1477	21	C48471	Arabidopsis thalia
C 153	15	2.7	1490	21	C35129	Arabidopsis thalia
C 154	15	2.7	1504	20	X26116	Arabidopsis thalia
C 155	15	2.7	1521	21	C77186	Fowlpox virus (FPV
C 156	15	2.7	1521	21	C42268	Human ORFX ORF2741
C 157	15	2.7	1562	21	C42467	Arabidopsis thalia
C 158	15	2.7	1591	20	X22715	Human cytochrome P
C 159	15	2.7	1613	20	X13448	Enterococcus faeca
C 160	15	2.7	1633	21	C93386	Human secreted pro
C 161	15	2.7	1640	12	O10990	Partial sequence o
C 162	15	2.7	1641	14	O49931	TNF-R cDNA. Homo
C 163	15	2.7	1641	15	O45224	Sequence encoding
C 164	15	2.7	1647	21	A40746	Wild type human CD
C 165	15	2.7	1656	20	X22125	Human secreted pro
C 166	15	2.7	1660	19	V48147	Nicotianamine amin
C 167	15	2.7	1704	21	C45181	Arabidopsis thalia
C 168	15	2.7	1720	19	Z96355	S. pneumoniae deri
C 169	15	2.7	1813	21	A79701	Eucalyptus grandis
C 170	15	2.7	1818	11	Q03599	Human liver cytoch
C 171	15	2.7	1820	21	A40755	Human cytochrome P
C 172	15	2.7	1823	20	Z33602	Wild type human CD
C 173	15	2.7	1845	20	X19925	Human breast tumo
C 174	15	2.7	1852	17	T11381	Mammalian cytochro
C 175	15	2.7	1852	19	V44157	Cytochrome P450 2C
C 176	15	2.7	1854	17	T11378	Human cytochrome P
C 177	15	2.7	1854	19	V44154	Cytochrome P450 2C
C 178	15	2.7	1865	20	V81212	Human cytochrome P
C 179	15	2.7	1870	13	Q21177	Human CD36 antigen
C 180	15	2.7	1870	17	T14716	Human CD36 antigen
C 181	15	2.7	1870	19	V63455	Human putative CD3
C 182	15	2.7	1870	21	A50591	Human CD36 antigen
C 183	15	2.7	1870	21	A40754	Human cell surface
C 184	15	2.7	1884	19	X14587	Wild type human CD
C 185	15	2.7	1910	21	C77329	H. pylori GHPO 169
C 186	15	2.7	1937	21	A47445	Human ORFX ORF2884
C 187	15	2.7	1938	21	C98184	Macaque TANGO 232
C 188	15	2.7	1942	21	A40753	Arabidopsis thalia
C 189	15	2.7	1948	21	C37986	Wild type human CD
C 190	15	2.7	1953	20	X55621	Arabidopsis thalia
C 191	15	2.7	2004	20	X55616	Sequence of mouse
C 192	15	2.7	2022	21	C44132	Sequence of mouse
C 193	15	2.7	2058	21	C98184	zeta mays DNA fragm
C 194	15	2.7	2092	20	X84370	Human colon cancer
C 195	15	2.7	2119	21	A09302	Drosophila Acp76A
C 196	15	2.7	2188	21	F16163	Human NIK1 protein
C 197	15	2.7	2198	21	A97937	Human prostate can
C 198	15	2.7	2214	21	A26448	Mung bean alpha 1,
C 199	15	2.7	2216	21	A40752	Human secreted pro
C 200	15	2.7	2224	16	O89544	Wild type human CD
C 201	15	2.7	2224	20	X55615	p75 Tumour Necrosi
C 202	15	2.7	2227	21	A26365	Sequence of mouse
C 203	15	2.7	2251	20	X55608	Human secreted pro
C 204	15	2.7	2251	20	X55609	Mouse clone 65 pro
C 205	15	2.7	2265	20	X26288	Mouse clone 65 ant
C 206	15	2.7	2339	12	O10956	Human RPL1 8392 ce
C 207	15	2.7	2339	20	Z09171	Encodes human 75kD
C 208	15	2.7	2365	18	V74406	Human tumour necro
C 209	15	2.7	2367	20	Z41998	Staphylococcus aur
C 210	15	2.7	2393	12	O10907	Human endometrium
C 211	15	2.7	2394	22	C83951	40kD TNF inhibitor
C 212	15	2.7	2402	20	X26119	Human 40 kDa TNF 1
C 213	15	2.7	2417	21	F16127	DNA sequence of FP
C 214	15	2.7	2478	20	X80148	Human prostate can
C 215	15	2.7	2488	18	V74418	Clostridium histol
C 216	15	2.7	2511	21	F21040	Staphylococcus aur
C 217	15	2.7	2511	21	A34918	Human low adenosin
C 218	15	2.7	2536	21	Z87186	Human adenosine re
C 219	15	2.7	2561	21	A40727	Human Brn1lac cDN
C 220	15	2.7	2561	21	A40745	Wild type human CD
C 221	15	2.7	2569	21	C93383	Human secreted pro
C 222	15	2.7	2684	20	Z10170	Human secreted pro
C 223	15	2.7	2745	19	V66367	cDNA encoding a hu
C 224	15	2.7	2792	22	F32738	Human cardiac and
C 225	15	2.7	2794	21	C93393	Human secreted pro
C 226	15	2.7	2828	12	Q15171	Human secreted pro
C 227	15	2.7	2829	21	Z93333	Bacillus thuringie
C 228	15	2.7	2853	22	F33096	Partial sequence o
C 229	15	2.7	3017	17	T36776	Human secreted pro
C 230	15	2.7	3017	17	T36786	Prostate-specific

C 231	15	2.7	3104	19	V68343	Transcriptional re
C 232	15	2.7	3106	20	X40172	WO9904265 Seq ID N
C 233	15	2.7	3198	21	F21093	Human low adenosin
C 234	15	2.7	3198	21	A34971	Human adenosine re
C 235	15	2.7	3226	21	A77665	Human PRO1154 cDNA
C 236	15	2.7	3326	21	Z65082	Membrane-bound pro
C 237	15	2.7	3417	21	A70163	Plasmodium falcipar
C 238	15	2.7	3432	20	X20281	Borrelia burgdorferi
C 239	15	2.7	3509	12	Q12287	Metallothionein-11
C 240	15	2.7	3567	18	T47559	42K promoted cytom
C 241	15	2.7	3567	21	A79309	42K promoted cytom
C 242	15	2.7	3657	19	V14015	Pinus radiata cell
C 243	15	2.7	3683	10	N90569	Xenopus paraxial p
C 244	15	2.7	4075	18	T47557	Ovine Y-chromosome
C 245	15	2.7	4075	20	X55618	42K promoted cytom
C 246	15	2.7	4909	18	T47558	Sequence of mouse
C 247	15	2.7	4909	22	F24165	42K promoted cytom
C 248	15	2.7	5727	18	V74501	Human secreted pro
C 249	15	2.7	6252	18	V74361	Staphylococcus aur
C 250	15	2.7	6560	20	X26118	Staphylococcus aur
C 251	15	2.7	6561	20	X26117	DNA sequence of PP
C 252	15	2.7	6645	20	X13432	DNA sequence of PP
C 253	15	2.7	6749	18	T47564	Enterococcus faeca
C 254	15	2.7	6749	18	T47561	Cytomegalovirus pp
C 255	15	2.7	7143	21	A70250	Cytomegalovirus pp
C 256	15	2.7	7722	21	A70168	Plasmodium falcipa
C 257	15	2.7	14078	18	V74502	Staphylococcus aur
C 258	15	2.7	15692	20	X24731	Plasmodium falcipa
C 259	15	2.7	15692	20	X24732	London-FAD APP tar
C 260	15	2.7	15701	20	X24733	Swedish-FAD APP713
C 261	15	2.7	16357	21	Z89337	Human UCP3 protein
C 262	15	2.7	16484	20	X13095	Enterococcus faeca
C 263	15	2.7	16595	21	F21095	Human low adenosin
C 264	15	2.7	16595	21	A34973	Human adenosine re
C 265	15	2.7	18436	19	V52220	Streptococcus pneu
C 266	15	2.7	21636	21	A55966	Human G713 3'-end
C 267	15	2.7	28720	19	V49655	Human SC3 DNA. Ho
C 268	15	2.7	32768	20	X12954	Enterococcus faeca
C 269	15	2.7	40138	20	V81946	V. marinus PKS-11k
C 270	15	2.7	40138	21	A71520	MAGE-B cluster DNA
C 271	15	2.7	40352	19	V02032	Polyomphic repeat
C 272	15	2.7	50000	21	A96366	Pg1 genomic coding
C 273	15	2.7	56516	20	Z00870	Wild type PGI codi
C 274	15	2.7	56520	20	Z01022	WFS1 variant genom
C 275	15	2.7	67212	21	A08954	BAC containing rep
C 276	15	2.7	83390	21	F22283	BAC containing rep
C 277	15	2.7	90336	21	F22289	Borrelia burgdorferi
C 278	15	2.7	111309	20	X20250	Human kinesin-like
C 279	15	2.7	121162	21	C66548	Human kinesin-like
C 280	15	2.7	144460	21	Z93815	Olfactory receptor
C 281	15	2.7	163319	21	F22306	Arabidopsis thalia
C 282	15	2.7	163319	21	F22306	Arabidopsis thalia
C 283	15	2.7	235033	19	V57926	Hereditary haemoch
C 284	15	2.7	235033	19	V57926	Hereditary haemoch
C 285	15	2.7	237326	19	V57903	Hereditary haemoch
C 286	15	2.7	237326	19	V57903	Hereditary haemoch
C 287	15	2.7	1038602	20	Z01425	Complete genome se
C 288	15	2.7	1082138	21	F22305	Arabidopsis thalia
C 289	15	2.7	1664976	19	V21205	Methanococcus jann
C 290	15	2.7	1830121	17	T42063	Haemophilus influ
C 291	15	2.5	18	15	Q35292	Cry j 1 cDNA PCR a
C 292	14	2.5	18	18	T80795	Staphylococcus aur
C 293	14	2.5	21	20	Z21760	Exemplary oligonuc
C 294	14	2.5	22	21	A55981	Human G713 PCR pri
C 295	14	2.5	22	14	A55955	HBV target sequenc
C 296	14	2.5	24	19	V19293	H. insulems celluli
C 297	14	2.5	24	21	Z35203	Olestin 16 kDa pro
C 298	14	2.5	25	13	Q34369	Upstream PCR prime
C 299	14	2.5	34	17	V32683	DEAD-box gene PCR
C 300	14	2.5	38	17	T10486	Human wild-type p5
C 301	14	2.5	38	18	T88442	5' PCR primer 3 (s
C 302	14	2.5	41	20	X89736	ClO502 Synthetic o
C 303	14	2.5	54	13	Q33976	Sequence upstream
C 304	14	2.5	55	16	Q74095	Human SDF-1-alpha
C 305	14	2.5	66	18	T69955	Entomopox 42K prom
C 306	14	2.5	71	18	V77639	Staphylococcus aur
C 307	14	2.5	72	22	C87459	Sendai virus PCR p
C 308	14	2.5	72	22	C87460	Sendai virus PCR p
C 309	14	2.5	72	22	C87511	Sendai virus PCR p
C 310	14	2.5	72	22	C87512	Sendai virus PCR p
C 311	14	2.5	92	18	T69951	F1VY matrix (M) ge
C 312	14	2.5	95	13	Q35796	42 KD promoter/F g
C 313	14	2.5	99	18	T47624	42 KD promoter/F g
C 314	14	2.5	104	14	Q37812	Sequence of an alt
C 315	14	2.5	104	19	V42680	Alternative exon f
C 316	14	2.5	104	21	A71698	Human calcium chan
C 317	14	2.5	107	13	Q35838	42 KD promoter. S
C 318	14	2.5	107	14	Q35405	Ameyv 42 KD promot
C 319	14	2.5	110	14	Q33138	Ameyv 42 K promote
C 320	14	2.5	115	21	A45604	Human secreted exp
C 321	14	2.5	119	16	T21518	Human gene signatu
C 322	14	2.5	125	17	T21866	Oligonucleotide se
C 323	14	2.5	129	16	T25190	Human gene signatu
C 324	14	2.5	132	21	C18469	Human secreted pro
C 325	14	2.5	135	17	T07239	Immunogen DNA from
C 326	14	2.5	150	4	N30069	Sequence of subseq
C 327	14	2.5	150	7	N60978	Fragment AI is a p
C 328	14	2.5	150	20	X05169	Human MSH5 (MMSH5)
C 329	14	2.5	172	21	C30131	Human secreted pro
C 330	14	2.5	178	21	C24722	Human secreted pro
C 331	14	2.5	181	21	Z89006	Human retina-spei
C 332	14	2.5	182	21	C13797	Human secreted pro
C 333	14	2.5	185	21	A69279	Human secreted pro
C 334	14	2.5	204	21	C15762	Bacteriophage Dp-1
C 335	14	2.5	205	17	T33989	Human secreted pro
C 336	14	2.5	208	21	C27902	Mouse neuropeptide
C 337	14	2.5	215	16	T25943	Human secreted pro
C 338	14	2.5	217	19	X12192	Human gene signatu
C 339	14	2.5	222	21	A42945	Human diallelic po
C 340	14	2.5	228	21	C21462	Human secreted exp
C 341	14	2.5	231	20	X41416	Human secreted pro
C 342	14	2.5	234	21	C17443	Human secreted pro
C 343	14	2.5	239	21	C04359	Human secreted pro
C 344	14	2.5	241	21	C00645	Human secreted pro
C 345	14	2.5	242	20	X40492	Human secreted pro
C 346	14	2.5	251	19	X11662	Human secreted pro
C 347	14	2.5	251	19	X12841	Human diallelic po
C 348	14	2.5	252	22	C90271	Human diallelic po
C 349	14	2.5	256	16	T21908	Partial mouse SNOR
C 350	14	2.5	257	21	C05901	Human gene signatu
C 351	14	2.5	265	21	A42012	Human secreted pro
C 352	14	2.5	271	21	C15080	Human secreted exp
C 353	14	2.5	274	16	T24164	Human gene signatu
C 354	14	2.5	278	21	C04249	Human gene signatu
C 355	14	2.5	289	21	Z42583	Human secreted pro
C 356	14	2.5	292	21	A45872	Human 5' EST isolat
C 357	14	2.5	300	20	Z14563	Human secreted exp
C 358	14	2.5	300	21	A01189	Human gene express
C 359	14	2.5	300	21	A01306	Human colon cancer
C 360	14	2.5	301	18	V77372	Human gene signatu
C 361	14	2.5	301	21	C04627	Staphylococcus aur
C 362	14	2.5	301	21	A06483	Human secreted pro
C 363	14	2.5	302	21	C17281	Human immunogenic
C 364	14	2.5	305	20	C10353	Human secreted pro
C 365	14	2.5	305	20	C00517	An intron/exon seq
C 366	14	2.5	306	20	X85728	Novel cDNA sequenc
C 367	14	2.5	311	21	C03592	Human secreted pro
C 368	14	2.5	311	21	C25061	Human secreted pro
C 369	14	2.5	314	21	A42039	Human secreted pro
C 370	14	2.5	322	16	T24879	Human gene signatu
C 371	14	2.5	333	21	A69234	Bacteriophage Dp-1
C 372	14	2.5	342	14	Q40891	T-BM gene sequenc
C 373	14	2.5	348	21	C28276	Human secreted pro
C 374	14	2.5	352	21	F21977	Human breast and o
C 375	14	2.5	359	21	C29367	Human secreted pro
C 376	14	2.5	394	21	C26408	Human secreted pro

377	14	2.5	395	21	A44539	Human secreted exp	c 450	14	2.5	650	20	V86942	EST clone BK61. H
378	14	2.5	399	21	C94093	Cat flea head and	451	14	2.5	650	21	Z80589	Human colon cancer
379	14	2.5	400	18	V75836	Staphylococcus aur	452	14	2.5	651	21	C54978	Arabidopsis thalia
380	14	2.5	400	18	V78383	Staphylococcus aur	453	14	2.5	653	21	C52439	Arabidopsis thalia
381	14	2.5	400	21	A26853	Essential Staphylo	454	14	2.5	654	21	F08474	Fusarium venenatum
382	14	2.5	402	21	F08639	Fusarium venenatum	455	14	2.5	655	21	C47658	Arabidopsis thalia
383	14	2.5	405	18	V75577	Staphylococcus aur	456	14	2.5	656	21	A98448	Roe deer PTEV/MMAC
384	14	2.5	406	21	C03312	Human secreted pro	457	14	2.5	657	21	A98859	Human proliferatio
385	14	2.5	407	21	C57423	Archidonic acid m	458	14	2.5	657	21	A98141	Human proliferatio
386	14	2.5	407	21	C57939	Archidonic acid m	459	14	2.5	667	21	Z80594	Human colon cancer
387	14	2.5	420	20	X89751	Synthetic DNA frag	460	14	2.5	672	21	F22110	Arabidopsis thalia
388	14	2.5	430	21	A44086	Human secreted exp	461	14	2.5	680	18	X30844	Streptococcus pneu
389	14	2.5	432	21	C13224	Human secreted pro	462	14	2.5	682	21	A68099	Plus radiata calf
390	14	2.5	434	19	V22113	Candida IFM5773 mi	463	14	2.5	686	18	T84074	DNA encoding a Sta
391	14	2.5	434	19	V22113	Candida IFM5800 mi	464	14	2.5	688	21	F14580	Aspergillus oryzae
392	14	2.5	439	18	V77953	Staphylococcus aur	465	14	2.5	696	18	V04437	Interleukin 4 rece
393	14	2.5	441	21	C02544	Human secreted pro	466	14	2.5	699	20	Z28259	Rat neuronal limed
394	14	2.5	446	21	C27989	Human secreted pro	467	14	2.5	702	21	C48336	Arabidopsis thalia
395	14	2.5	449	19	V73606	H. pylori caga DNA	468	14	2.5	704	21	C34079	Arabidopsis thalia
396	14	2.5	450	21	C79348	Plant viral moveme	469	14	2.5	705	21	C46491	Arabidopsis thalia
397	14	2.5	454	21	C04071	Human secreted pro	470	14	2.5	707	21	C34713	Arabidopsis thalia
398	14	2.5	459	14	Q48618	Cpg depleted gpt g	471	14	2.5	711	21	A47148	Arabidopsis thalia
399	14	2.5	461	16	T19904	Human gene signalu	472	14	2.5	720	21	F12664	DNA encoding the m
400	14	2.5	464	16	O86543	Wilson disease exo	473	14	2.5	724	21	F11860	Aspergillus oryzae
401	14	2.5	472	21	C21427	Human secreted pro	474	14	2.5	725	21	Z97446	Human prostate can
402	14	2.5	475	7	N60226	Sequence encoding	475	14	2.5	728	21	C3858	Arabidopsis thalia
403	14	2.5	475	7	N60226	Sequence encoding	476	14	2.5	732	20	C17594	Human gene express
404	14	2.5	478	21	V88421	Est clone EL360.	477	14	2.5	746	21	Z97445	Human prostate can
405	14	2.5	479	21	C43562	Zea mays DNA fragm	478	14	2.5	748	21	A78518	Human gene express
406	14	2.5	487	21	F11130	Fusarium venenatum	479	14	2.5	749	20	Z17441	Plant SDF polynuci
407	14	2.5	488	21	A57265	Human breast cance	480	14	2.5	752	21	A78486	Human gene express
408	14	2.5	489	21	C43316	Arabidopsis thalia	481	14	2.5	756	20	Z17111	Human gene express
409	14	2.5	489	21	C10151	Arabidopsis thalia	482	14	2.5	759	20	X99513	Nucleic acid seque
410	14	2.5	491	21	C36609	Human secreted pro	483	14	2.5	760	22	F22467	Human breast cance
411	14	2.5	495	21	F10963	Arabidopsis thalia	484	14	2.5	768	20	Z33517	Human prostate can
412	14	2.5	508	21	V86428	Fusarium venenatum	485	14	2.5	774	20	X99052	Human validated ca
413	14	2.5	513	20	V87757	Est clone AR467.	486	14	2.5	777	19	X14303	H. pylori GHP0 70
414	14	2.5	514	18	T80799	Staphylococcus aur	487	14	2.5	783	19	V38999	Exemplary CD40 lig
415	14	2.5	515	18	X20817	Polynucleotide seq	488	14	2.5	783	19	V42184	Exemplary nucleoti
416	14	2.5	517	20	X20846	Polynucleotide seq	489	14	2.5	786	21	C39655	Arabidopsis thalia
417	14	2.5	523	21	C55705	Human differentiat	490	14	2.5	786	15	O63959	Human CD40-L type
418	14	2.5	524	20	Z09015	Differentiation in	491	14	2.5	786	19	V46279	A. thaliana NIM-1
419	14	2.5	525	21	F14765	Aspergillus oryzae	492	14	2.5	786	19	V38997	CD40 ligand gene u
420	14	2.5	526	21	C34077	Arabidopsis thalia	493	14	2.5	786	19	V39002	Exemplary CD40 lig
421	14	2.5	543	20	X20858	Polynucleotide seq	494	14	2.5	786	19	V43665	Non-Inducible immu
422	14	2.5	548	21	C71142	Single nucleotide	495	14	2.5	786	19	V12852	CD40 ligand coding
423	14	2.5	549	21	C93877	Cat flea hindgut a	496	14	2.5	786	21	A01868	Human colon cancer
424	14	2.5	549	21	C93877	Cat flea hindgut a	497	14	2.5	791	19	V53452	DNA encoding a Sta
425	14	2.5	549	21	C93877	Cat flea hindgut a	498	14	2.5	798	18	V74928	Staphylococcus aur
426	14	2.5	553	20	X13524	Enterococcus faeca	499	14	2.5	798	20	Z77451	Human ovarian tumo
427	14	2.5	557	18	T83802	DNA encoding a Sta	500	14	2.5	799	21	C38896	Arabidopsis thalia
428	14	2.5	574	21	C00999	Human secreted pro	501	14	2.5	822	20	X84978	Human secreted pro
429	14	2.5	578	21	C72646	Single nucleotide	502	14	2.5	839	21	A40576	Human fetal placen
430	14	2.5	578	21	C72685	Single nucleotide	503	14	2.5	840	14	O41506	CD40-L. DNA. Homo
431	14	2.5	578	21	C72685	Single nucleotide	504	14	2.5	840	15	O57984	Genomic sequence o
432	14	2.5	581	21	C52354	Arabidopsis thalia	505	14	2.5	840	15	O67123	CD40 ligand gene.
433	14	2.5	585	21	A15914	Human protein clon	506	14	2.5	840	16	T05763	Human CD40 ligand
434	14	2.5	585	22	C92249	PERV-MSN1 pol regi	507	14	2.5	840	16	O94091	Human CD40-L. CDNA.
435	14	2.5	586	21	A16134	Human colon cancer	508	14	2.5	840	18	T93782	CDNA of CD40L, a n
436	14	2.5	586	22	C92248	PERV-MSN1 pol regi	509	14	2.5	840	18	T58132	Human CD40L. mutain
437	14	2.5	590	21	C50370	Arabidopsis thalia	510	14	2.5	840	19	Z26467	S. pneumoniae derl
438	14	2.5	590	22	C92250	PERV-MSN1 pol regi	511	14	2.5	840	19	V61053	Human CD40 ligand
439	14	2.5	593	18	X30892	Streptococcus pneu	512	14	2.5	840	20	Z27525	Human CD40-L. codin
440	14	2.5	593	21	C34261	Arabidopsis thalia	513	14	2.5	866	21	A78488	Plant SDF polynuci
441	14	2.5	600	20	V86185	EST clone J635. H	514	14	2.5	880	19	X14588	H. pylori GHP0 170
442	14	2.5	603	18	T67670	H. pylori cytoplas	515	14	2.5	889	11	O04528	Replication initia
443	14	2.5	606	19	V42183	Exemplary nucleoti	516	14	2.5	894	19	T98730	DNA encoding a S.
444	14	2.5	609	6	N50090	Sequence encoding	517	14	2.5	894	21	C37201	Arabidopsis thalia
445	14	2.5	620	16	T05790	Human CD40 ligand	518	14	2.5	900	7	N60506	0.9 Kbp segment of
446	14	2.5	620	21	C45150	Arabidopsis thalia	519	14	2.5	900	17	V09008	KSHV assembly prot
447	14	2.5	621	20	X99586	Nucleic acid seque	520	14	2.5	904	18	V74321	Staphylococcus aur
448	14	2.5	641	21	D00433	Human MIM15 DNA c	521	14	2.5	906	11	O05975	Sequence encoding
449	14	2.5	642	19	X30601	H. pylori cellular	522	14	2.5	906	21	C77681	Human cancer assoc

523	14	2.5	908	21	C74382	Human secreted pro
C 524	14	2.5	914	21	C47666	Arabidopsis thalia
C 525	14	2.5	915	19	V09009	KSHV assembly prot
526	14	2.5	919	18	V74871	Staphylococcus aur
C 527	14	2.5	923	21	C42604	Arabidopsis thalia
C 528	14	2.5	930	17	T36784	Prostate-specific
C 529	14	2.5	932	20	V84471	Human secreted pro
C 530	14	2.5	941	13	O29856	Odorant receptor c
C 531	14	2.5	975	21	C42291	Arabidopsis thalia
C 532	14	2.5	979	21	A94088	Fruit-associated b
C 533	14	2.5	989	21	A50292	Candida albicans C
C 534	14	2.5	987	21	C45393	Arabidopsis thalia
C 535	14	2.5	1000	20	Z15900	Human gene express
C 536	14	2.5	1000	20	Z15901	Human gene express
C 537	14	2.5	1001	22	C88189	Optimum primer can
C 538	14	2.5	1009	21	C41101	Arabidopsis thalia
C 539	14	2.5	1015	16	T04076	M.gallisepticum DN
540	14	2.5	1017	17	T41625	Adzuki bean xylogl
541	14	2.5	1018	14	Q36929	HEV1 cDNA clone.
C 542	14	2.5	1024	21	Z97146	Human prostate can
543	14	2.5	1025	9	N80304	Sequence of cDNA c
544	14	2.5	1030	21	C78042	Human cancer assoc
545	14	2.5	1031	22	C90276	Mouse SNORF3 rece
546	14	2.5	1035	16	T04705	PCSPOLY5A fragment
C 547	14	2.5	1036	20	Z17349	Human gene express
C 548	14	2.5	1037	20	X84975	Human secreted pro
549	14	2.5	1047	18	T84182	DNA encoding a sta
550	14	2.5	1047	19	V53521	DNA encoding a sta
551	14	2.5	1049	21	C37987	Arabidopsis thalia
C 552	14	2.5	1054	11	Q06112	Sequence encoding
C 553	14	2.5	1070	18	T59195	Clone PT218 contai
C 554	14	2.5	1070	20	Z29901	Nucleotide sequenc
C 555	14	2.5	1070	21	Z48591	N. tabacum cryptic
C 556	14	2.5	1074	21	A94091	Fusion sequence of
557	14	2.5	1076	21	A68179	Bacteriophage Dp-1
C 558	14	2.5	1079	17	T36068	Chicken gamma inte
559	14	2.5	1081	21	A97924	A. thaliana PUP1 D
560	14	2.5	1087	20	X19424	Nicotiana tabacum
C 561	14	2.5	1096	19	V07891	Nucleotide sequenc
562	14	2.5	1101	22	C90246	Rat SNORF3 recept
563	14	2.5	1106	13	O29663	Sugar beet acidic
C 564	14	2.5	1111	11	Q05671	Uncoupling protein
C 565	14	2.5	1111	11	Q08578	UCP messenger RNA.
C 566	14	2.5	1115	10	N90125	cDNA encoding IGE
C 567	14	2.5	1119	21	C53578	Arabidopsis thalia
C 568	14	2.5	1127	17	T41618	Human ORFX ORF2201
C 569	14	2.5	1127	20	Z21221	Ze mays eIF-4E pr
570	14	2.5	1128	20	Z24655	Human lung tumor a
571	14	2.5	1128	21	C65894	Human lung cancer-
572	14	2.5	1128	21	C46094	Arabidopsis thalia
573	14	2.5	1130	21	C31166	Arabidopsis thalia
574	14	2.5	1131	21	C76646	Human ORFX ORF2201
575	14	2.5	1139	11	Q06249	Phospholipase D to
576	14	2.5	1140	21	C33314	Arabidopsis thalia
577	14	2.5	1149	21	C51073	Arabidopsis thalia
C 578	14	2.5	1149	21	A39968	Murine TANGO 186 c
C 579	14	2.5	1155	21	C49626	Arabidopsis thalia
C 580	14	2.5	1156	20	X76974	Histamine binding
C 581	14	2.5	1159	21	C39510	Arabidopsis thalia
582	14	2.5	1173	15	O67883	Murine p53 DNA. S
583	14	2.5	1173	20	Z32518	Myrbean cyclin-dep
584	14	2.5	1173	20	Z08528	Murine p53 gene.
C 585	14	2.5	1174	21	C52054	Arabidopsis thalia
C 586	14	2.5	1175	11	O04088	Bod4-15 insert enc
587	14	2.5	1175	21	A05567	Streptococcus pneu
C 588	14	2.5	1176	20	X61405	DNA encoding a hum
C 589	14	2.5	1194	18	V74433	Staphylococcus aur
590	14	2.5	1194	19	V46278	A. thaliana C- and
C 591	14	2.5	1194	19	V43664	Non-inducible immu
C 592	14	2.5	1194	21	Z51529	S. paucimobilis am
C 593	14	2.5	1202	13	O25060	PSbeta1a-318 clone
C 594	14	2.5	1212	20	Z28298	Rat neuronal immed
595	14	2.5	1217	21	A51362	Streptococcus agal
C 596	14	2.5	1220	20	X84956	Human secreted pro
597	14	2.5	1223	18	V74891	Staphylococcus aur
C 598	14	2.5	1225	22	F44488	Mouse dextran sodi
C 599	14	2.5	1231	20	Z28265	Rat neuronal immed
600	14	2.5	1234	21	C77698	Human cancer assoc
601	14	2.5	1234	21	C49818	Arabidopsis thalia
C 602	14	2.5	1235	17	O33062	Encodes Babesia bo
C 603	14	2.5	1242	17	T18993	Babesia merozoite
604	14	2.5	1242	21	C79768	Human secreted pro
605	14	2.5	1247	21	C35991	Arabidopsis thalia
606	14	2.5	1271	18	T95020	Arabidopsis JAG18
C 607	14	2.5	1281	21	C43477	Arabidopsis thalia
C 608	14	2.5	1281	21	C56341	Pinus radiata tran
C 609	14	2.5	1293	21	C45019	Arabidopsis thalia
C 610	14	2.5	1303	21	A95345	Aspergillus polyke
611	14	2.5	1310	20	Z24656	Human lung tumor a
612	14	2.5	1310	21	C65895	Human lung cancer-
613	14	2.5	1317	15	Q71601	Japanese cedar pol
C 614	14	2.5	1333	21	C44915	Arabidopsis thalia
615	14	2.5	1337	14	O35304	Cry j I gene. Cry
616	14	2.5	1337	15	O55271	Cry j I gene. Cry
617	14	2.5	1337	16	T04248	Cry j I Japanese C
C 618	14	2.5	1343	22	F33131	Human secreted pro
619	14	2.5	1348	21	F18332	Lung cancer associ
620	14	2.5	1348	21	Z24205	S. aureus sarA reg
C 621	14	2.5	1353	17	T41701	Murine lymphocyte
622	14	2.5	1356	21	Z39863	Plasmodium malaria
623	14	2.5	1358	18	T84705	Human renin cDNA.
624	14	2.5	1358	21	C49566	Arabidopsis thalia
C 625	14	2.5	1368	14	Q38448	Arabidopsis thalia
626	14	2.5	1372	21	C33629	Arabidopsis thalia
C 627	14	2.5	1375	21	C51920	Arabidopsis thalia
C 628	14	2.5	1378	21	C42223	Arabidopsis thalia
629	14	2.5	1387	14	O53419	Mycoplasma gallise
630	14	2.5	1387	15	O77854	Mycoplasma gallise
631	14	2.5	1387	16	O94711	Mycoplasma gallise
632	14	2.5	1388	17	T18168	CORC potassium cha
633	14	2.5	1389	12	O14918	CD46 clone pm5.3.
634	14	2.5	1389	20	Z17120	Human gene express
635	14	2.5	1395	21	C75776	Human ORFX ORF1331
636	14	2.5	1396	21	C54561	Arabidopsis thalia
637	14	2.5	1401	18	T95022	Arabidopsis thalia
638	14	2.5	1401	21	C33196	DNA flanking the T
639	14	2.5	1419	21	C49392	Arabidopsis thalia
640	14	2.5	1419	21	C49393	Arabidopsis thalia
641	14	2.5	1425	21	F11620	Arabidopsis thalia
642	14	2.5	1431	12	Q14917	Aspergillus niger
643	14	2.5	1441	19	V43594	CD46 clone pm5.10.
644	14	2.5	1443	18	T80793	Arabidopsis chloro
645	14	2.5	1443	19	V53427	Staphylococcus aur
646	14	2.5	1455	21	C46079	DNA encoding a sta
647	14	2.5	1457	21	C33676	Arabidopsis thalia
648	14	2.5	1459	6	N50180	Arabidopsis thalia
649	14	2.5	1463	21	C39968	Sequence encoding
C 650	14	2.5	1472	21	C50136	Arabidopsis thalia
651	14	2.5	1477	18	T90306	Human MCP cDNA. H
C 652	14	2.5	1477	21	C33778	Arabidopsis thalia
653	14	2.5	1484	19	V18254	Arabidopsis thalia
654	14	2.5	1487	21	C40181	Human growth-induc
C 655	14	2.5	1505	18	T72177	Arabidopsis thalia
C 656	14	2.5	1505	21	C47413	Alzheimer's diseas
657	14	2.5	1510	21	C34975	Arabidopsis thalia
658	14	2.5	1512	19	V68995	Arabidopsis thalia
659	14	2.5	1512	21	C81006	DNA molecule encod
660	14	2.5	1512	21	A06593	Human BILAG1 anti
661	14	2.5	1515	21	A70162	Human immunofalci
C 662	14	2.5	1515	21	C50415	Plasmodium falcipa
663	14	2.5	1518	21	A02658	Arabidopsis thalia
C 664	14	2.5	1523	21	C38003	Human colon cancer
665	14	2.5	1533	21	O99106	Arabidopsis thalia
666	14	2.5	1530	16	Q99106	Human MCP (CD46) F
C 667	14	2.5	1533	18	T87066	Human CD46 cDNA.
C 668	14	2.5	1533	20	X08478	Bovine platelet-ac

c 669	14	2.5	1533	20	V08552	Bovine PAF-AH codi	c 742	14	2.5	1863	21	248290	Bacillus sp. Aa386
c 670	14	2.5	1533	21	A59594	CDNA encoding plat	c 743	14	2.5	1874	21	A57959	1875 bp Candida al
c 671	14	2.5	1533	21	C45930	Arabidopsis thalia	c 744	14	2.5	1887	22	F32699	Human secreted pro
c 672	14	2.5	1533	21	A10879	Bovine PAF-AH nucl	c 745	14	2.5	1917	21	F87239	DNA encoding nativ
c 673	14	2.5	1533	21	B24255	Bovine PAF-AH cDNA	c 746	14	2.5	1923	21	C74722	Arabidopsis thalia
c 674	14	2.5	1533	22	C89072	Platelet-activatin	c 747	14	2.5	1925	21	A94092	Fusion sequence of
c 675	14	2.5	1533	21	C35232	Arabidopsis thalia	c 748	14	2.5	1925	21	C38450	Arabidopsis thalia
c 676	14	2.5	1539	21	C42990	Arabidopsis thalia	c 749	14	2.5	1931	19	B26385	S. pneumoniae deri
c 677	14	2.5	1542	21	C45040	Arabidopsis thalia	c 750	14	2.5	1933	21	A23442	CDNA encoding huma
c 678	14	2.5	1544	21	C34726	Arabidopsis thalia	c 751	14	2.5	1943	7	N60965	Autonomously repli
c 679	14	2.5	1546	12	O10864	Sequence encoding	c 752	14	2.5	1948	21	A09312	Human cancer assoc
c 680	14	2.5	1551	20	V84612	Human secreted pro	c 753	14	2.5	1950	20	X86149	DNA encoding a Bac
c 681	14	2.5	1564	20	Z08962	Human neokine-1 CD	c 754	14	2.5	1962	20	B25934	Human prostate tum
c 682	14	2.5	1579	17	T44594	AF1q CDNA involved	c 755	14	2.5	1962	20	B25934	Human prostate tum
c 683	14	2.5	1590	19	V09014	KSHV protease/asse	c 756	14	2.5	1975	11	O05057	Drai/Drai fragment
c 684	14	2.5	1594	21	C53583	Arabidopsis thalia	c 757	14	2.5	1977	17	T36794	Prostate-specific
c 685	14	2.5	1597	19	V46276	A. thaliana N-term	c 758	14	2.5	1980	20	X40197	Sequence of C3Vs 9
c 686	14	2.5	1597	19	V43662	Non-inducible immu	c 759	14	2.5	1986	7	N60595	2.0 Kbp segment of
c 687	14	2.5	1605	19	V09016	KSHV protease/asse	c 760	14	2.5	1991	12	O14916	CD46 clone pm5.6.
c 688	14	2.5	1608	19	V46277	A. thaliana C-term	c 761	14	2.5	1992	14	O48591	Alcohol oxidase ge
c 689	14	2.5	1608	19	V43663	Non-inducible immu	c 762	14	2.5	2001	18	T59700	pH-like peptide D
c 690	14	2.5	1608	21	A57988	1608 bp Candida al	c 763	14	2.5	2001	21	A26941	Essential Staphylo
c 691	14	2.5	1608	21	Z44680	Human IFN-gamma DN	c 764	14	2.5	2007	21	A39967	Murine TANGO 186 c
c 692	14	2.5	1608	22	C87635	Bovine beta-L,4-N-	c 765	14	2.5	2011	19	A39967	A. thaliana NIM-1
c 693	14	2.5	1610	18	T59911	Yeast transcriptio	c 766	14	2.5	2011	19	V46274	Non-inducible immu
c 694	14	2.5	1610	21	C79774	Human secreted pro	c 767	14	2.5	2011	19	V43661	Arabidopsis thalia
c 695	14	2.5	1619	20	X13500	Enterococcus faeca	c 768	14	2.5	2023	21	C49400	Arabidopsis thalia
c 696	14	2.5	1622	18	V75043	Staphylococcus aur	c 769	14	2.5	2024	21	C37765	Arabidopsis thalia
c 697	14	2.5	1627	20	X13633	Enterococcus faeca	c 770	14	2.5	2042	21	A52773	Soybean putative c
c 698	14	2.5	1629	21	C48405	Arabidopsis thalia	c 771	14	2.5	2042	21	A52773	Arabidopsis thalia
c 699	14	2.5	1630	20	Z42039	Human endometrium	c 772	14	2.5	2043	20	X59526	Human CDNA encodin
c 700	14	2.5	1630	20	Z42039	Human endometrium	c 773	14	2.5	2043	20	X59526	Interleukin-1 beta
c 701	14	2.5	1631	19	X14344	H. pylori GHPD 265	c 774	14	2.5	2065	22	F32645	Fusion polypeptide
c 702	14	2.5	1638	20	X84991	Human secreted pro	c 775	14	2.5	2071	19	V46494	Fusion polypeptide
c 703	14	2.5	1639	18	V74661	Staphylococcus aur	c 776	14	2.5	2076	21	A09044	Arabidopsis thalia
c 704	14	2.5	1643	21	A87754	Human secreted pro	c 777	14	2.5	2084	21	B25242	Human secreted pro
c 705	14	2.5	1643	21	B25150	Human Cathepsin S	c 778	14	2.5	2085	21	A09043	Fusion polypeptide
c 706	14	2.5	1659	12	O14915	CD46 clone pm5.1.	c 779	14	2.5	2104	19	V16851	Arabidopsis thalia
c 707	14	2.5	1659	21	C69476	Human secreted pro	c 780	14	2.5	2105	21	B29336	A. thaliana gene 1
c 708	14	2.5	1668	21	A72926	Human secreted pro	c 781	14	2.5	2115	19	V38373	Beta(1 -> 4)-N-ace
c 709	14	2.5	1685	20	Z42035	Human PRO273 nucle	c 782	14	2.5	2116	17	T31024	1-Sucrose:sucrose
c 710	14	2.5	1685	21	C78551	Human PRO273 (UNO2-	c 783	14	2.5	2133	12	O14966	Varicella Zoster V
c 711	14	2.5	1689	21	C58588	Human PRO273 prote	c 784	14	2.5	2134	12	C84183	A. thaliana shorte
c 712	14	2.5	1689	20	Z40803	Secreted protein E	c 785	14	2.5	2137	20	V82824	Mouse GP88 autocori
c 713	14	2.5	1690	20	X04614	Genomic sequence e	c 786	14	2.5	2140	21	Z49411	Pea DRR206 protein
c 714	14	2.5	1701	19	V09015	KSHV protease/asse	c 787	14	2.5	2158	21	C93483	Human secreted pro
c 715	14	2.5	1710	21	C39470	Arabidopsis thalia	c 788	14	2.5	2161	19	V29573	S. thermophilus FI
c 716	14	2.5	1749	16	O91211	TF55 molecular cha	c 789	14	2.5	2181	20	X56461	Human SVPH1-26 pro
c 717	14	2.5	1750	20	X30400	DNA encoding a hum	c 790	14	2.5	2204	21	Z43753	CDNA encoding a hu
c 718	14	2.5	1752	21	C75773	Human OREF ORF1328	c 791	14	2.5	2207	20	X03845	Human NNK3 CDNA.
c 719	14	2.5	1760	21	C59930	Human secreted pro	c 792	14	2.5	2220	14	O33008	Novel intestinal o
c 720	14	2.5	1767	21	C46909	Arabidopsis thalia	c 793	14	2.5	2222	18	V74993	Scaphylococcus aur
c 721	14	2.5	1776	18	T67912	H. pylori cytoplasm	c 794	14	2.5	2226	19	V38368	Human endometrium
c 722	14	2.5	1779	21	A49185	CDNA encoding huma	c 795	14	2.5	2246	20	Z42116	Beta(1 -> 4)-N-ace
c 723	14	2.5	1785	20	X99656	Nucleic acid seque	c 796	14	2.5	2259	14	O46782	40 kDa and 34 kDa
c 724	14	2.5	1785	20	X99656	Human endometrium	c 797	14	2.5	2259	21	C42350	Arabidopsis thalia
c 725	14	2.5	1801	21	C36220	Arabidopsis thalia	c 798	14	2.5	2267	21	C59489	Human secreted pro
c 726	14	2.5	1813	21	C39494	Arabidopsis thalia	c 799	14	2.5	2276	18	T84929	Human secreted pro
c 727	14	2.5	1816	21	A51745	Human CPA0 ligand	c 800	14	2.5	2276	18	T84929	Human secreted pro
c 728	14	2.5	1821	19	V22736	Babesia microti BM	c 801	14	2.5	2276	18	T84929	Human secreted pro
c 729	14	2.5	1821	20	X89000	Babesia microti an	c 802	14	2.5	2329	21	A05501	Human prostate pr
c 730	14	2.5	1821	21	C65083	B. microti BMN1-6	c 803	14	2.5	2294	18	T60957	CDNA encoding a pr
c 731	14	2.5	1821	21	C65083	Human secreted pro	c 804	14	2.5	2302	21	C76368	Streptococcus pneu
c 732	14	2.5	1827	21	F22379	Human secreted pro	c 805	14	2.5	2309	15	O73786	Malize tapetum-spec
c 733	14	2.5	1838	21	C59703	DNA molecule encod	c 806	14	2.5	2329	21	C76368	Human OREF ORF1923
c 734	14	2.5	1853	19	V68996	Human B11Aq1 antiq	c 807	14	2.5	2332	20	X03844	Partial PCR fragme
c 735	14	2.5	1853	21	C81007	Human immunogenic	c 808	14	2.5	2332	20	X03844	Human 7-transmembr
c 736	14	2.5	1853	21	A06584	DNA molecule encod	c 809	14	2.5	2340	20	X80866	Human nucleic acid
c 737	14	2.5	1855	19	V68998	Maize cell death s	c 810	14	2.5	2346	15	O77857	Myoplasma gallise
c 738	14	2.5	1855	21	C81009	Human B11Aq1 antiq	c 811	14	2.5	2355	21	A09049	Human secreted pro
c 739	14	2.5	1855	21	A06596	Human immunogenic	c 812	14	2.5	2356	20	X90696	IL-13/IL-4 dual tr
c 740	14	2.5	1855	21	A06596	Human immunogenic	c 813	14	2.5	2356	20	X90696	Human Cytoplasmic
c 741	14	2.5	1862	21	A59972	Bovine calictonin	c 814	14	2.5	2356	20	X90696	Human Cytoplasmic

C 815	14	2.5	2374	18	T96816	DNA encoding LysC,
C 816	14	2.5	2382	21	A09050	IL-13/IL-4 dual tr
C 817	14	2.5	2393	21	Z46135	CDNA encoding an a
C 818	14	2.5	2400	20	X25372	Staphylococcus aure
C 819	14	2.5	2409	19	V19377	Humicola insolens
C 820	14	2.5	2409	19	V19281	H. insolens celluli
C 821	14	2.5	2426	20	X28636	Nucleotide sequenc
C 822	14	2.5	2441	15	O55144	Enterococcus faeca
C 823	14	2.5	2449	21	A63952	CDNA encoding a hu
C 824	14	2.5	2453	21	A94087	Fruit-associated b
C 825	14	2.5	2459	21	C75871	Human ORF1426
C 826	14	2.5	2459	21	A12406	CDNA encoding a hu
C 827	14	2.5	2470	18	T72944	Phaffia carotenoid
C 828	14	2.5	2475	11	O04307	Coding region of h
C 829	14	2.5	2475	18	T61551	Human interleukin-
C 830	14	2.5	2475	19	V38331	Human interleukin-
C 831	14	2.5	2475	19	V17656	Human interleukin-
C 832	14	2.5	2475	20	X22408	Human IL-4 recepto
C 833	14	2.5	2475	20	V08857	Human interleukin-
C 834	14	2.5	2513	21	X3813	Coding sequence fo
C 835	14	2.5	2513	21	A79275	Pinus radiata cell
C 836	14	2.5	2520	21	A46789	DNA encoding a mam
C 837	14	2.5	2520	21	Z50939	Soluble Interleuk
C 838	14	2.5	2525	21	Z98026	Human secreted pro
C 839	14	2.5	2532	21	Z87218	DNA encoding nativ
C 840	14	2.5	2539	17	T46075	Human activated le
C 841	14	2.5	2539	19	V13954	Activated leukocyt
C 842	14	2.5	2541	21	A59346	Nucleotide sequenc
C 843	14	2.5	2541	18	T72941	Phaffia carotenoid
C 844	14	2.5	2559	20	Z09236	Human B3 ubiquitin
C 845	14	2.5	2559	18	T88850	Neuronal activity-
C 846	14	2.5	2613	19	V26280	Botulinum neurotox
C 847	14	2.5	2616	19	V26291	Recombinant botuli
C 848	14	2.5	2616	19	V26291	Recombinant botuli
C 849	14	2.5	2622	19	V26288	Recombinant botuli
C 850	14	2.5	2627	20	Z77559	Human ovarian tumo
C 851	14	2.5	2628	19	V26281	Recombinant botuli
C 852	14	2.5	2637	19	V26282	Recombinant botuli
C 853	14	2.5	2646	21	C42283	Arabidopsis thalia
C 854	14	2.5	2651	18	T47539	42K promoted cytom
C 855	14	2.5	2651	20	X13369	Enterococcus faeca
C 856	14	2.5	2674	21	C77146	Human ORF2701
C 857	14	2.5	2685	19	V26287	Recombinant botuli
C 858	14	2.5	2724	19	V26284	Recombinant botuli
C 859	14	2.5	2730	22	C84293	Human EXCS encodin
C 860	14	2.5	2783	20	Z33566	Human breast tumou
C 861	14	2.5	2784	21	A30850	Chlamydia antigen
C 862	14	2.5	2804	21	C77708	Human cancer assoc
C 863	14	2.5	2807	21	A11389	Mucor circinelloid
C 864	14	2.5	2815	20	X06817	Chlamydia pneumoni
C 865	14	2.5	2820	21	C79730	Human secreted pro
C 866	14	2.5	2822	20	X52222	Protein PRO228 cDN
C 867	14	2.5	2822	21	A54097	PRO228 CDNA, Homo
C 868	14	2.5	2822	21	Z93701	PRO288 DNA32092-12
C 869	14	2.5	2822	22	C97429	Human angiotensin
C 870	14	2.5	2830	20	Z27909	Canine B7-1 protei
C 871	14	2.5	2830	20	Z27910	Canine B7-1 gene c
C 872	14	2.5	2853	21	C77970	Human cancer assoc
C 873	14	2.5	2858	21	A58011	2858 bp Candida al
C 874	14	2.5	2862	19	V26283	Recombinant botuli
C 875	14	2.5	2875	18	T47713	Mouse bone morphog
C 876	14	2.5	2934	21	C98826	Human pancreatic c
C 877	14	2.5	2937	21	C59340	Human secreted pro
C 878	14	2.5	2940	20	V65173	A. thaliana trehal
C 879	14	2.5	2946	20	V34005	Human Rab3-GAP gen
C 880	14	2.5	2948	20	V08568	S. aureus D-alanin
C 881	14	2.5	2950	21	A30849	Chlamydia antigen
C 882	14	2.5	2969	21	A23450	CDNA encoding huma
C 883	14	2.5	2970	20	X20290	Borrelia burgdorfe
C 884	14	2.5	2987	21	Z94785	Human SGP CDNA.
C 885	14	2.5	2989	18	T69956	FLPV matrix (M) ge
C 886	14	2.5	2995	19	V70355	Human h-NUMB encod
C 887	14	2.5	2995	20	V64417	Mouse developing l
C 888	14	2.5	2999	21	C78119	Human cancer assoc
C 889	14	2.5	3000	20	X06828	Chlamydia pneumoni
C 890	14	2.5	3024	14	O39260	ICAM-1 CDNA, Homo
C 891	14	2.5	3035	19	X14059	H. pylori GHPo 325
C 892	14	2.5	3042	19	V26285	Recombinant botuli
C 893	14	2.5	3058	20	X90695	Human Cytoplasmic
C 894	14	2.5	3063	10	N91438	DNA encoding glyci
C 895	14	2.5	3065	16	O90942	Murine wild type p
C 896	14	2.5	3091	21	C99028	Human pancreatic c
C 897	14	2.5	3097	17	T28951	Human secreted pro
C 898	14	2.5	3126	14	O42425	ADRA3 DNA, Synhel
C 899	14	2.5	3140	21	Z93814	Subtilase (St_P25c
C 900	14	2.5	3159	18	V74614	Staphylococcus aur
C 901	14	2.5	3172	21	A63854	Nucleotide sequenc
C 902	14	2.5	3184	22	C84184	A. thaliana larges
C 903	14	2.5	3188	5	N40244	Hepatitis virus ad
C 904	14	2.5	3214	11	O05377	Fragment of plasm
C 905	14	2.5	3215	21	Z37088	Nucleotide sequenc
C 906	14	2.5	3218	18	T60328	Beta-casein promot
C 907	14	2.5	3271	18	V74747	Staphylococcus aur
C 908	14	2.5	3288	16	T05055	Human transforming
C 909	14	2.5	3308	21	F18270	Lung cancer associ
C 910	14	2.5	3350	21	Z40700	Human EGFR polype
C 911	14	2.5	3355	20	X36342	Human TIE ligand N
C 912	14	2.5	3355	21	A77529	Human PRO188 CDNA
C 913	14	2.5	3355	22	C97379	Human angiogenesis
C 914	14	2.5	3411	17	T28950	Helicobacter-spect
C 915	14	2.5	3423	21	C45759	Arabidopsis thalia
C 916	14	2.5	3508	21	A16619	Human secreted pro
C 917	14	2.5	3539	18	T47537	42K promoted cytom
C 918	14	2.5	3546	21	C42844	Arabidopsis thalia
C 919	14	2.5	3550	18	T72946	Phaffia carotenoid
C 920	14	2.5	3555	22	F27737	Human transport pr
C 921	14	2.5	3561	15	O67667	Delta endotoxin ge
C 922	14	2.5	3561	18	T89184	Nematoe toxin 807
C 923	14	2.5	3561	18	T77277	Bacillus thuringie
C 924	14	2.5	3561	18	T61017	Bacillus thuringie
C 925	14	2.5	3567	21	A70117	Plasmodium falcipa
C 926	14	2.5	3580	20	V81742	Human PP04 encodi
C 927	14	2.5	3592	21	A26912	Essential staphylo
C 928	14	2.5	3597	21	F20977	Human low adenosin
C 929	14	2.5	3597	21	A34855	Human adenosine re
C 930	14	2.5	3600	20	X25180	Hiv-1 group O isol
C 931	14	2.5	3616	19	V00245	Rat Ret ligand ret
C 932	14	2.5	3649	6	N50416	Calf acetyl cholin
C 933	14	2.5	3654	16	T72326	Lactobacillus bact
C 934	14	2.5	3661	16	T05902	Human IL-2 gene (p
C 935	14	2.5	3691	20	X06408	Tumour suppressor
C 936	14	2.5	3691	20	X99691	Nucleic acid sequ
C 937	14	2.5	3692	20	Z27237	Human secreted pro
C 938	14	2.5	3705	21	A53826	Sequence encoding
C 939	14	2.5	3711	21	C77143	Human ORF ORF2698
C 940	14	2.5	3714	21	A51777	S. cerevisiae esse
C 941	14	2.5	3738	21	A70178	Plasmodium falcipa
C 942	14	2.5	3747	21	C49587	Arabidopsis thalia
C 943	14	2.5	3792	21	C88443	Thiamine responsi
C 944	14	2.5	3815	18	T84154	DNA encoding one k
C 945	14	2.5	3815	19	V53496	DNA encoding a Sta
C 946	14	2.5	3822	20	X91737	Porphyromonas ging
C 947	14	2.5	3823	21	A59529	Nucleotide sequenc
C 948	14	2.5	3835	11	O05378	Sequence of hepati
C 949	14	2.5	3846	20	X91736	Porphyromonas ging
C 950	14	2.5	3853	21	C77598	Human ORF ORF3153
C 951	14	2.5	3891	17	T29244	C. botulinum type
C 952	14	2.5	3936	20	X91609	Porphyromonas ging
C 953	14	2.5	3950	21	A38929	Cotton delta-cadin
C 954	14	2.5	4002	21	Z24153	Murine PG-Lb DNA.
C 955	14	2.5	4018	18	X60126	Sequence of introm
C 956	14	2.5	4071	18	T68658	Mycoplasma pneumo
C 957	14	2.5	4144	14	O37188	Mouse fosB coding
C 958	14	2.5	4184	19	V41259	Mouse neuronal p45
C 959	14	2.5	4193	16	O82834	Human strumalin-2
C 960	14	2.5	4219	18	V74523	Staphylococcus aur

C 961	14	2.5	4230	21	A51328	Human E3 ubiquitin
C 962	14	2.5	4313	20	Z34349	Human PRO31 nucle
C 963	14	2.5	4313	21	C78562	Human PRO31 (UNQ3
C 964	14	2.5	4319	17	T117215	Adhesion and penet
C 965	14	2.5	4323	21	C46790	Arbidopsis thaila
C 966	14	2.5	4365	21	Z38917	Neisseria meningit
C 967	14	2.5	4427	18	T47538	42k promoted cytom
C 968	14	2.5	4433	18	T95023	Arabidopsis thaila
C 969	14	2.5	4659	11	Q01491	DNA sequence encod
C 970	14	2.5	4702	18	V74579	Staphylococcus aur
C 971	14	2.5	4703	21	C76621	Human ORF ORP2176
C 972	14	2.5	4756	16	O86541	Wilson disease gen
C 973	14	2.5	4835	21	C64582	BONT/A neurotoxin
C 974	14	2.5	4837	18	V74469	Staphylococcus aur
C 975	14	2.5	4838	20	V70891	Plasmid pRK-esp-La
C 976	14	2.5	4886	21	C76173	Arbidopsis thaila
C 977	14	2.5	4893	18	T47560	Human ORF ORP1728
C 978	14	2.5	5032	19	V39129	Cytomegalovirus gh
C 979	14	2.5	5052	21	C50830	Polydeptide having
C 980	14	2.5	5062	18	T47569	Arbidopsis thaila
C 981	14	2.5	5173	18	T89783	CMV gL gene, trunc
C 982	14	2.5	5194	20	X25885	Human Immunodefici
C 983	14	2.5	5224	21	Z32973	C.albicans alpha-I
C 984	14	2.5	5313	19	V24562	Human wild-type pr
C 985	14	2.5	5372	20	Z09325	Plasmid pMB430 con
C 986	14	2.5	5391	19	V71729	Human E3 ubiquitin
C 987	14	2.5	5407	19	V71738	Upstream sequence
C 988	14	2.5	5421	16	O85678	Wilson's disease g
C 989	14	2.5	5423	18	V74535	Staphylococcus aur
C 990	14	2.5	5440	21	A97522	Plasmid pUC/35S.C4
C 991	14	2.5	5518	18	T73870	Cotton fibre promo
C 992	14	2.5	5521	18	V74719	Staphylococcus aur
C 993	14	2.5	5529	21	Z98680	Barley endoxylanase
C 994	14	2.5	5547	18	T73865	Cotton fibre promo
C 995	14	2.5	5555	21	C77191	Human ORF ORP2746
C 996	14	2.5	5561	21	F20964	Human low adenosin
C 997	14	2.5	5561	21	A34842	Human adenosine re
C 998	14	2.5	5566	21	A55967	Human G713 encodin
C 999	14	2.5	5622	20	V49587	Arabidopsis AG11 g
C 1000	14	2.5	5635	19	V46273	A. thaliana NIM-1

## ALIGNMENTS

RESULT	1
T799321	
ID	T799321 standard; DNA; 555 BP.
XX	
AC	T799321;
XX	
DT	16-FEB-1998 (first entry)
XX	
DE	DNA encoding <i>Staphylococcus marinus</i> esterase Fl-12LC.
XX	
KM	Esterase; thermostable enzyme; ester; chiral compound;
KM	pulp; paper; lignin removal; sugar; lignocellulose;
KM	disease resistance; feedstuff; ss.
XX	
OS	<i>Staphylococcus marinus</i> strain Fl.
XX	
Key	Location/Qualifiers
FT	1..576
FT	/*tag= a
FT	/transl_except= (pos: 526..528, aa:asp
PN	W09730160-A1.
XX	
PD	21-AUG-1997.
XX	
PF	11-FEB-1997; 97W0-US02039.
XX	
DR	16-FEB-1996; 96US-0602359.

[illegible]



QY 481 CCCGAGTTATTAACCGGATTCCTCGTTTTTACACTCTATATAAGACAGTATTTTAAVCA 540  
 |||  
 DB 481 ccgagttatcagcgatctcgttttaccattctataagaacagatatttaac 540  
 QY 541 TACACTAAGCATAG 555  
 |||  
 DB 541 tacactaaacagata 555

## RESULT 2

T79300/C  
 ID T79300 standard; cDNA; 31 BP.

AC T79300;

DT 17-FEB-1998 (first entry)

DE Staphylothermus marinus esterase Fl-12LC gene 3' PCR primer.

KW Esterase; thermostable enzyme; ester; chiral compound; cheese;

KM pulp; paper; lignin removal; sugar; lignocellulose;

KM disease resistance; feedstuff; primer; PCR; ss.

OS Synthetic.

OS Staphylothermus marinus strain F1.

PN MO9730160-A1.

PD 21-AUG-1997.

PF 11-FEB-1997; 97WO-US02039.

PR 16-FEB-1996; 96US-0602359.

PI (RECO-) RECOMBINANT BIOCATALYSIS INC.

PI Callen W, Kosmotka A, Link S, Maffia AM, Murphy D;

PI Reid J, Robertson DE, Swanson RV, Warren PV;

DR WPI; 1997-425035/39.

PS Nucleic acid encoding heat stable esterase from thermophilic

CC bacteria - which is active in organic solvents, useful in cheese or

CC paper manufacture, and to study plant resistance to disease

CC Example 1; Page 28; 113pp; English.

CC A 3' PCR primer (T79300) and a 5' PCR primer (T79299) can be used

CC to amplify the esterase Fl-12LC gene (see T79321) of

CC Staphylothermus marinus F1 from a pBluescript vector containing

CC the DNA. The amplified sequence can then be inserted into a pOET

CC vector, and the esterase (see W23069-88) are provided in bacterial host

CC cells. Novel esterases (see W23069-88) are provided that are

CC stable at high temperature and in organic solvents, making them

CC superior for use in production of pure chiral compounds used in

CC the pharmaceutical, agricultural and other chemical industries.

XX Sequence 31 BP; 7 A; 4 C; 7 G; 13 T; 0 other;

Query Match 3.88; Score 21; DB 18; Length 31;

Best Local Similarity 100.0%; Pred. No. 0.39;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 535 AATCATACACTAAGCATAG 555

DB 31 AATCATACACTAAGCATAG 11

## RESULT 3

T79299  
 ID T79299 standard; cDNA; 52 BP.

XX T79299;  
 AC  
 XX  
 DT 17-FEB-1998 (first entry)  
 XX

DE Staphylothermus marinus esterase Fl-12LC gene 5' PCR primer.

KW Esterase; thermostable enzyme; ester; chiral compound; cheese;

KM pulp; paper; lignin removal; sugar; lignocellulose;

KM disease resistance; feedstuff; primer; PCR; ss.

OS Synthetic.

OS Staphylothermus marinus strain F1.

PN MO9730160-A1.

PD 21-AUG-1997.

PF 11-FEB-1997; 97WO-US02039.

PR 16-FEB-1996; 96US-0602359.

PI (RECO-) RECOMBINANT BIOCATALYSIS INC.

PI Callen W, Kosmotka A, Link S, Maffia AM, Murphy D;

PI Reid J, Robertson DE, Swanson RV, Warren PV;

DR WPI; 1997-425035/39.

PS Nucleic acid encoding heat stable esterase from thermophilic

CC bacteria - which is active in organic solvents, useful in cheese or

CC paper manufacture, and to study plant resistance to disease

CC Example 1; Page 28; 113pp; English.

CC A 5' PCR primer (T79299) and a 3' PCR primer (T79300) can be used

CC to amplify the esterase Fl-12LC gene (see T79321) of

CC Staphylothermus marinus F1 from a pBluescript vector containing

CC the DNA. The amplified sequence can then be inserted into a pOET

CC vector, and the esterase (see W23069-88) are provided in bacterial host

CC cells. Novel esterases (see W23069-88) are provided that are

CC stable at high temperature and in organic solvents, making them

CC superior for use in production of pure chiral compounds used in

CC the pharmaceutical, agricultural and other chemical industries.

XX Sequence 52 BP; 21 A; 9 C; 8 G; 14 T; 0 other;

Query Match 3.88; Score 21; DB 18; Length 52;

Best Local Similarity 100.0%; Pred. No. 0.38;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTTTAAACAGCACTCT 21

DB 32 atgctttaacaagcactct 52

## RESULT 4

V52181/C  
 ID V52181 standard; DNA; 25002 BP.

AC V52181;

DT 23-OCT-1998 (first entry)

DE Streptococcus pneumoniae genome fragment SEQ ID NO:48.

KW Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;

KM computer readable medium; vaccine; pharmaceutical composition; ds.

OS Streptococcus pneumoniae.

PN WO9818931-A2.

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XX 07-MAY-1998.
PD 30-OCT-1997; 97WO-US19588.
XX 31-OCT-1996; 96US-0029960.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M;
PI Kunsch CA, Rosen CA;
XX WPI; 1998-272225/24.
XX Computer-readable medium with recorded Streptococcus pneumoniae
XX polynucleotide sequences - useful in diagnostic kits and assays, and
XX pharmaceutical compositions and vaccines for Streptococcus
XX pneumoniae
XX Claim 1; Page 431-445; 1409pp; English.
XX The present invention describes a computer readable medium which has
XX the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded
XX on it, or a representative fragment of a sequence at least 95% identical
XX to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1
XX to 391 (V52134 to V52524) are genomic fragments from Streptococcus
XX pneumoniae. The present invention also describes an isolated nucleic acid
XX molecule encoding a homologue of any of the fragments of the S. pneumoniae
XX genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced
XX by a process comprising: (a) screening a genomic DNA library using as a
XX probe a target sequence defined by any of the sequences in SEQ ID NO:1
XX to 391, identifying members of the library which contain sequences
XX that hybridize to the target sequence and isolating the nucleic acid
XX molecules from the members; or (b) isolating mRNA, DNA or cDNA produced
XX from an organism, amplifying nucleic acid molecules whose nucleotide
XX sequence is homologous to amplification primers derived from the
XX fragment of the S. pneumoniae genome to prime the amplification and
XX isolating the amplified sequences. The computer readable medium can be
XX used in a computer-based system for identifying fragments of the
XX S. pneumoniae genome of commercial importance, or expression modulating
XX fragments of the S. pneumoniae genome. Products from the present
XX invention can be used in diagnosis kits and assays, and pharmaceutical
XX compositions and vaccines for S. pneumoniae.
XX Sequence 25002 BP; 7422 A; 5498 C; 4618 G; 7463 T; 1 other;
SQ
Query Match 3.2%; Score 18; DB 19; Length 25002;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 182 TTGCAATTGGTGGATAC 199
DB 17016 TTGCAATTGGTGGATAC 16999
RESULT 5
X83005/c
ID X83005 standard; DNA; 29604 BP.
AC X83005;
XX 31-AUG-1999 (first entry)
XX Partial mouse WRN genomic sequence #1.
XX Mouse: WRN; Werner's syndrome; detection; diagnosis; autosomal;
XX recessive disorder; phenotype; ss.
XX Mus musculus.
XX W09724435-A1.
XX

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PD 10-JUL-1997.
XX 30-DEC-1996; 96WO-US20785.
XX 12-APR-1996; 96US-0632175.
XX 29-DEC-1995; 95US-0009409.
XX 29-DEC-1995; 95US-0580539.
XX 30-JAN-1996; 96US-0010835.
XX 30-JAN-1996; 96US-0594242.
XX (DARW-) DARWIN MOLECULAR CORP.
XX (OSHU/) OSHIMA J.
XX Fu Y, Mulligan J, Oshima J, Schellenberg GD, Yu C;
XX WPI; 1997-363671/33.
XX Isolated nucleic acid molecule encoding the WRN gene product
XX useful for detection and treatment of Werner's syndrome, and related
XX diseases
XX Claim 1; Fig 7; 153pp; English.
XX This sequence represents a fragment of the genomic sequence containing
XX the coding region for the mouse WRN gene (X83004). The corresponding
XX human gene (X83001) encodes a protein related to Werner's syndrome.
XX The products can be used for the detection and treatment of Werner's
XX syndrome (WS), an autosomal recessive disorder with a complex phenotype,
XX as well as related diseases.
XX Sequence 29604 BP; 7634 A; 5861 C; 5985 G; 10123 T; 1 other;
SQ
Query Match 3.2%; Score 18; DB 18; Length 29604;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 99 ATGGTTTAATATATGGA 116
DB 29176 ATGGTTTAATATATGGA 29159
RESULT 6
X52014
ID X52014 standard; DNA; 157 BP.
AC X52014;
XX 22-JUN-1999 (first entry)
XX Human secreted protein 5' EST SEQ ID NO: 228.
XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
XX forensic; gene therapy; chromosome mapping; signal peptide;
XX upstream regulatory sequence; cytokine activity; cell proliferation;
XX differentiation; haematopoiesis regulation; tissue growth regulation;
XX reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
XX thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX Homo sapiens.
XX W09906552-A2.
XX 11-FEB-1999.
XX 31-JUL-1998; 98WO-1B01236.
XX 01-AUG-1997; 97US-0905223.
XX (GSEST ) GENSET.
XX Duclert A, Dumas Milne Edwards J, Lacroix B;
XX

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XX Dumas MLine Edwards J, Duclert A, Giordano J;
PI WPI: 2000-500381/45.
XX P-PSDB: G03846.
DR New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX Claim 1: SEQ ID 3850; 71bp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC derived from 30 different tissues. EST sequences usually correspond
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC well suited for isolating cDNA sequences derived from the 5' ends of
CC mRNAs and even in those cases where longer cDNA sequences have been
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC mRNAs with intact 5' ends and can therefore be used to obtain full length
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures. They are used to obtain
CC upstream regulatory sequences and to design expression and secretion
CC vectors.
XX
SQ Sequence 361 BP; 124 A; 50 C; 74 G; 113 T; 0 other;

Query Match          3.1%; Score 17; DB 21; Length 361;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 TGTATAGTTGGTTTAA 220
   |||||||||||||||
DB 247 tgtatagttggtttaa 263

RESULT 9
T26471 ID T26471 standard; cDNA to mRNA; 422 BP.
XX
AC T26471;
XX
DT 23-OCT-1996 (first entry)
XX
DE Human gene signature HUMGS08713.
XX
KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KM human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
XX
OS Homo sapiens.
XX
PN W09514772-A1.
XX
PD 01-JUN-1995.
XX
PF 11-NOV-1994; 94WO-JP01916.
XX
PR 12-NOV-1993; 93JP-0355504.
XX
PA (MATS/) MATSUBARA K.
XX (OKUB/) OKUBO K.
XX
PI Matsubara K, Okubo K;
XX
DR WPI: 1995-206931/27.
XX
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human

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PT tissues
XX
XX Claim 1: Page 2094; 2245bp; Japanese.
XX
CC A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in T19001-T26837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.
XX
SQ Sequence 422 BP; 112 A; 70 C; 83 G; 142 T; 15 other;

Query Match          3.1%; Score 17; DB 16; Length 422;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 TGTATAGTTGGTTTAA 220
   |||||||||||||||
DB 138 tgtatagttggtttaa 154

RESULT 10
C35823/c ID C35823 standard; DNA; 486 BP.
XX
AC C35823;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays DNA fragment SEQ ID NO: 11554.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.

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PR 06-MAY-1999; 99US-0132486.  
 PR 06-MAY-1999; 99US-0132487.  
 PR 07-MAY-1999; 99US-0132863.  
 PR 11-MAY-1999; 99US-0134256.  
 PR 14-MAY-1999; 99US-0134218.  
 PR 14-MAY-1999; 99US-0134219.  
 PR 14-MAY-1999; 99US-0134221.  
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 PR 10-JUN-1999; 99US-0138540.  
 PR 14-JUN-1999; 99US-0138847.  
 PR 16-JUN-1999; 99US-0139119.  
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 PR 31-AUG-1999; 99US-0151438.  
 PR 01-SEP-1999; 99US-0151930.  
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 PR 28-SEP-1999; 99US-0156458.  
 PR 29-SEP-1999; 99US-0156596.  
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 PR 08-OCT-1999; 99US-0158222.  
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 PR 14-OCT-1999; 99US-0159637.  
 PR 14-OCT-1999; 99US-0159638.  
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 PR 21-OCT-1999; 99US-0160770.

PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
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PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 3.1%; Score 17; DB 21; Length 486;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 AGCTGTGCTCAATAT 170  
|||||  
DB 218 AGCTGTGCTCAATAT 202

RESULT 11  
C94715/c  
ID C94715 standard; cDNA: 498 BP.  
AC C94715;  
XX  
DT 19-FEB-2001 (first entry)  
XX  
DE Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:1210.  
XX  
KM Cat flea: hindgut and Malpighian tubule nucleic acid; HMT;  
KM flea infestation; vaccine; antiparasitic; therapeutic target;  
KM diagnosis; detection; ss.  
XX  
OS Ctenocephalides felis.  
XX  
PN WO200061621-A2.  
XX  
PD 19-OCT-2000.  
XX  
PF 07-APR-2000; 2000WO-US09437.  
XX  
PR 09-APR-1999; 99US-0128704.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;  
PI WPI: 2000-656323/63.  
XX  
DR WPI: 2000-656323/63.  
XX  
PT Flea Malpighian tubule and head and nerve cord tissue derived nucleic  
PT acids useful for the prevention, diagnosis and treatment of flea  
PT infestations -  
XX  
PS Claim 26: Page 636; 964pp; English.  
XX  
CC The invention relates to novel cat flea (Ctenocephalides felis) nucleic  
CC acids which are expressed in hindgut and Malpighian tubule (HMT) tissue  
CC or head and nerve cord (HNC) tissue. The invention also relates to the  
CC encoded proteins. The invention additionally encompasses expression  
CC constructs, recombinant viruses and recombinant cells comprising the  
CC nucleic acids of the invention, recombinant production of the proteins,  
CC antibodies against the proteins, a method of identifying inhibitors of  
CC the proteins, and compositions comprising the inhibitors for  
CC administration to an animal. The nucleic acids, and the proteins they  
CC encode may be used in the prevention, treatment and diagnosis of diseases  
CC associated with flea infestations. For example, the nucleic acids may be  
CC used to produce an HMT or HNC protein according to standard recombinant

CC DNA methodology by inserting the nucleic acids into a host cell and  
CC culturing the cell to express the protein. The HMT and HNC nucleic acids  
CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect  
CC and quantitate the presence of cat flea or other homologous nucleic acid  
CC sequences in samples. They may also be used to study the expression and  
CC function of the proteins and their role in metabolism. The HMT and HNC  
CC proteins may be used as antigens in the production of specific  
CC antibodies, and in assays to identify modulators (agonists and  
CC antagonists) of HMT and/or HNC protein expression and activity. The  
CC anti-HMT/HNC protein antibodies and antigens may also be used to  
CC downregulate protein expression and activity. The antibodies may also be  
CC used as diagnostic agents for detecting the presence of flea polypeptides  
CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The  
CC present sequence represents a cat flea HMT cDNA of the invention.  
XX  
SQ Sequence 498 BP; 179 A; 47 C; 74 G; 186 T; 12 other;

Query Match 3.1%; Score 17; DB 21; Length 498;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 ATTCTTACTTAATAG 292  
|||||  
DB 496 ATTCTTACTTAATAG 480

RESULT 12  
Z16638/c  
ID Z16638 standard; cDNA: 849 BP.  
AC Z16638;  
XX  
DT 12-OCT-1999 (first entry)  
XX  
DE Human gene expression product cDNA sequence SEQ ID NO:4108.  
XX  
KM Human; gene; gene expression product; diagnosis; therapy; probe;  
KM detection; mapping; tissue typing; profiling; forensic; cancer;  
KM genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9938972-A2.  
XX  
PD 05-AUG-1999.  
XX  
PF 28-JAN-1999; 99WO-US01619.  
XX  
PR 03-APR-1998; 98US-0080666.  
PR 28-JAN-1998; 98US-0072910.  
PR 24-FEB-1998; 98US-0075954.  
PR 31-MAR-1998; 98US-0080114.  
PR 03-APR-1998; 98US-0080515.  
XX  
PA (CHIR) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
XX  
PI Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;  
PI Escobedo J, Garcia PD, Garcia V, Gliese K, Innis MA;  
PI Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;  
PI Lamsan G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;  
PI Stache-Crain B, Sudduth-Klinger J, Williams LT;  
XX  
DR WPI: 1999-494092/41.  
XX  
PT Novel human genes and their expression products which are  
PT differentially expressed in different cell types  
XX  
PS Claim 1: Page 1947; 2479pp; English.  
XX  
CC The present invention describes a library of human polynucleotides  
CC comprising the sequences given in Z12532 to Z17779. Also described is a



PA (UWRO-) ROCKFELLER UNIV.  
 XX  
 PI Coruzzi GM, Tsai FY;  
 XX  
 DR WPI: 1990-361471/48.  
 XX  
 PT Plant asparagine synthetase - includes DNA expression system and  
 XX transgenic plants  
 PS  
 XX Claim 33: Fig 12: 91pp; English.  
 CC The promoter sequence corresponding to nucleotides 1 to 1031 is  
 CC used to control expression of as2 in transgenic plants. The  
 CC promoter is induced in cotyledons during germination, in nitrogen  
 CC fixing root nodules and in leaves, stem and roots by dark treat-  
 CC ment. The promoter and the as2 sequences can be cloned into  
 CC expression vectors to produce AS2 which can be used to engineer  
 CC herbicide resistance, as a dominant selectable marker, to select  
 CC novel herbicides or compounds useful for synchronising plant cells  
 CC in culture, etc.  
 CC See also Q06598, Q06599 and Q06622.  
 CC  
 SQ Sequence 1121 BP: 424 A; 156 G; 150 G; 388 T; 3 other:

Query Match 3.1%; Score 17; DB 11; Length 1121;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 336 AGTATTGTTTCTTAT 352  
 |||  
 DB 798 AGTATTGTTTCTTAT 782

## RESULT 15

A99072/c  
 ID A99072 standard; DNA: 1563 BP.

AC A99072;

DT 18-JAN-2001 (first entry)

DE Arabidopsis thaliana basl nucleotide sequence SEQ ID NO:1.

KW Arabidopsis thaliana: basl; promoter; cytochrome P450; CYP72B1; plant;  
 KM brassinosteroid signalling; brassinosteroid synthesis; brassinolide; ds.

OS Arabidopsis thaliana.

PN WO200055302-A2.

PD 21-SEP-2000.

PF 16-MAR-2000; 2000WO-US06915.

PR 16-MAR-1999; 99US-0124570.

PR 14-DEC-1999; 99US-0170931.

PR 20-DEC-1999; 99US-0172832.

PA (SALK ) SALK INST BIOLOGICAL STUDIES.

PI Neff MM, Chory J;

DR WPI: 2000-638195/61.

DR P-PSDB: B23917.

PT Transgenic plants having modulated brassinolide synthesis resulting in  
 PT insect resistance, dwarfism and darker-green foliage compared with  
 PT wild-type plants, have nucleic acid encoding Basl polypeptide in its  
 PT genome

PS Disclosure: Fig 1A; 104pp; English.

CC The present invention describes a genetically modified plant (I)  
 CC comprising at least one exogenous nucleic acid sequence encoding a Basl  
 CC polypeptide, homologue or functional fragment, in its genome or at least  
 CC one regulatory sequence that modified expression of endogenous basl  
 CC gene, homologue or functional fragment, and which is characterised as  
 CC having modulated brassinolide activity or synthesis. The basl gene  
 CC encodes a cytochrome P450 (CYP72B1), which has a role in brassinosteroid  
 CC signalling or synthesis. Overexpression of the basl gene in plants  
 CC causes a dark green, dwarf phenotype which mimics plants that have low  
 CC levels of the plant hormone, brassinolide. Overexpression of the basl  
 CC gene also increases resistance to insects in plants. The present  
 CC sequence represents the Arabidopsis basl nucleotide sequence, which is  
 CC used in the exemplification of the present invention.

SQ Sequence 1563 BP: 424 A; 310 G; 377 G; 452 T; 0 other:

Query Match 3.1%; Score 17; DB 21; Length 1563;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 402 AGCTGTTCTACTAATA 418  
 |||  
 DB 648 AGCTGTTCTACTAATA 632

Search completed: May 31, 2001, 02:17:19  
 Job time: 4480 sec







GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2001, 01:01:09 ; Search time 63.31 Seconds  
(without alignments)  
1530.635 Million cell updates/sec

Title: US-09-382-242-23  
Perfect score: 555  
Sequence: 1 ATGCTTTAAACAGACACTC.....AATCATACCTAAACGATAG 555

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 302621 seqs, 87301344 residues

Word size : 0

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued\_Patents\_NA:\*  
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3: /cgnl\_7/prodata/1/lna/5A\_COMB.seq:\*  
4: /cgnl\_7/prodata/1/lna/5B\_COMB.seq:\*  
5: /cgnl\_7/prodata/1/lna/PCTUS\_COMB.seq:\*  
6: /cgnl\_7/prodata/1/lna/backfillseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	100.0	555	2	US-08-602-359A-23
2	21	3.8	31	2	US-08-602-359A-2
3	18	3.2	29604	3	US-08-602-359A-1
4	17	3.1	1121	6	US-08-781-891-207
5	17	3.1	837	2	US-08-549-515-4
6	16	2.9	1700	2	US-08-897-340-4
7	16	2.9	1700	4	US-09-252-329-4
8	16	2.9	2483	1	US-08-464-340A-3
9	16	2.9	2483	5	PCT-US94-08449A-3
10	16	2.9	3386	1	US-08-703-809-2
11	16	2.9	3386	1	US-08-703-809-2
12	16	2.9	3386	1	US-08-703-809-2
13	16	2.9	3386	2	US-08-014-066-2
14	16	2.9	3386	2	US-08-703-807-2
15	16	2.9	3386	2	US-08-747-108A-2
16	16	2.9	3386	4	US-09-211-631-2
17	16	2.9	3386	4	US-09-265-628-2
18	16	2.9	3386	4	US-09-001-141-2
19	16	2.9	4051	3	US-08-549-515-1
20	15	2.7	580	1	US-08-322-962-3
21	15	2.7	580	3	US-08-450-653-3
22	15	2.7	1016	2	US-08-930-617-1
23	15	2.7	1178	2	US-08-933-750C-88
24	15	2.7	1178	4	US-09-234-613-88
25	15	2.7	1203	3	US-09-122-443-3
26	15	2.7	1419	2	US-08-194-981E-4
27	15	2.7	1591	2	US-08-194-981E-3

28	15	2.7	1641	1	US-08-385-229-1	Sequence 1, Appl
29	15	2.7	1641	2	US-08-650-000-1	Sequence 1, Appl
30	15	2.7	1641	6	5395760-1	Patent No. 5395760
31	15	2.7	1852	1	US-08-201-118-10	Sequence 10, Appl
32	15	2.7	1852	2	US-08-238-821B-10	Sequence 10, Appl
33	15	2.7	1852	5	PCT-US95-05744-10	Sequence 10, Appl
34	15	2.7	1854	1	US-08-201-118-4	Sequence 4, Appl
35	15	2.7	1854	2	US-08-238-821B-4	Sequence 4, Appl
36	15	2.7	1854	5	PCT-US95-05744-4	Sequence 4, Appl
37	15	2.7	1265	2	US-08-940-332-1	Sequence 2, Appl
38	15	2.7	2684	2	US-08-984-171-2	Sequence 2, Appl
39	15	2.7	2957	2	US-08-394-152A-48	Sequence 48, Appl
40	15	2.7	3017	2	US-08-394-152A-39	Sequence 39, Appl
41	15	2.7	3030	2	US-08-680-326-24	Sequence 24, Appl
42	15	2.7	3509	1	US-08-322-962-1	Sequence 1, Appl
43	15	2.7	3509	1	US-08-450-653-1	Sequence 1, Appl
44	15	2.7	3567	2	US-08-658-665-69	Sequence 69, Appl
45	15	2.7	3567	4	US-08-796-101-33	Sequence 63, Appl
46	15	2.7	3655	4	US-08-878-474-6	Sequence 67, Appl
47	15	2.7	4075	2	US-08-658-665-67	Sequence 31, Appl
48	15	2.7	4075	2	US-08-796-101-31	Sequence 68, Appl
49	15	2.7	4909	4	US-08-658-665-68	Sequence 32, Appl
50	15	2.7	4909	4	US-08-796-101-32	Sequence 71, Appl
51	15	2.7	6749	2	US-08-658-665-71	Sequence 177, Appl
52	15	2.7	6749	4	US-08-658-665-177	Sequence 35, Appl
53	15	2.7	6749	4	US-08-796-101-35	Sequence 38, Appl
54	15	2.7	6749	4	US-08-796-101-38	Sequence 12, Appl
55	15	2.7	40332	4	US-09-090-793-12	Sequence 15, Appl
56	15	2.7	40332	2	US-08-846-111D-15	Sequence 15, Appl
57	15	2.7	66516	2	US-08-996-306-1	Sequence 20, Appl
58	15	2.7	246240	2	US-08-724-394A-20	Sequence 20, Appl
59	15	2.7	246240	2	US-08-724-394A-20	Sequence 21, Appl
60	15	2.7	246240	2	US-08-724-394A-21	Sequence 21, Appl
61	15	2.7	246240	2	US-08-724-394A-21	Sequence 22, Appl
62	15	2.7	246240	2	US-08-724-394A-22	Sequence 22, Appl
63	15	2.7	246240	2	US-08-724-394A-22	Sequence 22, Appl
64	15	2.5	18	3	US-08-467-023-17	Sequence 12, Appl
65	14	2.5	24	3	US-08-193-627-30	Sequence 30, Appl
66	14	2.5	38	1	US-08-259-612A-2	Sequence 2, Appl
67	14	2.5	38	1	US-08-644-291-2	Sequence 115, Appl
68	14	2.5	46	2	US-08-658-665-115	Sequence 115, Appl
69	14	2.5	46	4	US-08-796-101-91	Sequence 94, Appl
70	14	2.5	54	4	US-08-658-665-118	Sequence 94, Appl
71	14	2.5	54	4	US-08-796-101-94	Sequence 18, Appl
72	14	2.5	55	1	US-08-323-084A-18	Sequence 8, Appl
73	14	2.5	55	1	US-08-674-008-18	Sequence 8, Appl
74	14	2.5	66	2	US-08-566-398-8	Sequence 376, App
75	14	2.5	95	1	US-08-566-398-4	Sequence 376, App
76	14	2.5	95	1	US-08-105-483-376	Sequence 167, App
77	14	2.5	95	1	US-08-709-209-376	Sequence 143, App
78	14	2.5	95	1	US-08-458-101-376	Sequence 143, App
79	14	2.5	99	2	US-08-658-665-167	Sequence 4, Appl
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81	14	2.5	104	1	US-07-745-206A-4	Sequence 2, Appl
82	14	2.5	104	1	US-08-455-43A-2	Sequence 2, Appl
83	14	2.5	104	2	US-08-193-078B-2	Sequence 2, Appl
84	14	2.5	104	2	US-08-223-095C-2	Sequence 2, Appl
85	14	2.5	104	2	US-08-149-097-2	Sequence 4, Appl
86	14	2.5	104	2	US-08-311-363-4	Sequence 2, Appl
87	14	2.5	104	3	US-08-949-386-2	Sequence 2, Appl
88	14	2.5	104	3	US-08-450-662-2	Sequence 435, App
89	14	2.5	107	1	US-08-105-483-435	Sequence 435, App
90	14	2.5	107	1	US-08-709-209-435	Sequence 143, App
91	14	2.5	107	1	US-08-408-325-143	Sequence 143, App
92	14	2.5	107	1	US-08-458-101-435	Sequence 143, App
93	14	2.5	110	6	5174993-18	Patent No. 5174993
94	14	2.5	110	6	5505941-18	Patent No. 5505941
95	14	2.5	135	2	US-08-611-757-21	Sequence 21, Appl
96	14	2.5	135	5	PCT-US95-05980-21	Sequence 14, Appl
97	14	2.5	342	5	PCT-US97-09955-14	Sequence 8, Appl
98	14	2.5	363	1	US-08-040-204-8	Sequence 4, Appl
99	14	2.5	400	3	US-08-714-918-4	Sequence 4, Appl
100	14	2.5	400	4	US-09-265-315-4	Sequence 4, Appl

C 101	14	2.5	400	US-09-265-315-4	Sequence 4, Appl1	174	14	2.5	1629	1	US-08-589-080-2	Sequence 2, Appl1
C 102	14	2.5	459	PCT-US93-01676A-7	Sequence 7, Appl1	175	14	2.5	1659	2	US-08-528-057-1	Sequence 1, Appl1
C 103	14	2.5	459	PCT-US93-01676A-8	Sequence 8, Appl1	176	14	2.5	1701	3	US-09-064-703-4	Sequence 4, Appl1
C 104	14	2.5	583	US-09-404-671-5	Sequence 5, Appl1	177	14	2.5	1749	1	US-08-116-098-1	Sequence 1, Appl1
C 105	14	2.5	583	US-09-404-671-7	Sequence 7, Appl1	178	14	2.5	1821	4	US-08-845-256-6	Sequence 6, Appl1
C 106	14	2.5	686	US-08-627-151A-12	Sequence 12, Appl1	179	14	2.5	1855	4	US-08-810-009-1	Sequence 1, Appl1
C 107	14	2.5	786	US-08-446-922-3	Sequence 15, Appl1	180	14	2.5	1862	3	US-09-238-796-1	Sequence 1, Appl1
C 108	14	2.5	786	US-08-989-478-15	Sequence 15, Appl1	181	14	2.5	1975	6	5436393-1	Sequence 43, Appl1
C 109	14	2.5	786	US-08-996-685-15	Sequence 15, Appl1	182	14	2.5	1986	2	US-08-485-288A-3	Sequence 3, Appl1
C 110	14	2.5	786	PCT-US93-10034-3	Sequence 3, Appl1	183	14	2.5	1992	1	US-08-714-918-92	Sequence 92, Appl1
C 111	14	2.5	809	US-09-276-531-27	Sequence 27, Appl1	184	14	2.5	2001	3	US-09-265-315-92	Sequence 92, Appl1
C 112	14	2.5	840	US-07-940-605A-1	Sequence 1, Appl1	185	14	2.5	2001	4	US-09-265-315-92	Sequence 92, Appl1
C 113	14	2.5	840	US-08-184-422-7	Sequence 7, Appl1	186	14	2.5	2001	4	US-09-265-315-92	Sequence 92, Appl1
C 114	14	2.5	840	US-08-360-923A-1	Sequence 1, Appl1	187	14	2.5	2011	2	US-08-989-478-6	Sequence 6, Appl1
C 115	14	2.5	840	US-08-431-055-3	Sequence 3, Appl1	188	14	2.5	2011	2	US-08-989-478-6	Sequence 6, Appl1
C 116	14	2.5	840	US-08-690-096-1	Sequence 1, Appl1	189	14	2.5	2011	3	US-08-996-685-6	Sequence 6, Appl1
C 117	14	2.5	840	US-08-249-189-11	Sequence 11, Appl1	190	14	2.5	2011	3	US-08-996-685-6	Sequence 6, Appl1
C 118	14	2.5	840	US-08-484-624A-11	Sequence 11, Appl1	191	14	2.5	2071	4	US-09-023-023-1	Sequence 1, Appl1
C 119	14	2.5	840	US-08-477-733B-11	Sequence 11, Appl1	192	14	2.5	2116	3	US-08-860-091A-1	Sequence 1, Appl1
C 120	14	2.5	840	US-08-763-995-1	Sequence 1, Appl1	193	14	2.5	2124	1	US-08-087-007-1	Sequence 1, Appl1
C 121	14	2.5	840	US-09-088-913A-11	Sequence 11, Appl1	194	14	2.5	2124	4	US-08-483-433-1	Sequence 1, Appl1
C 122	14	2.5	840	US-08-589-771B-7	Sequence 7, Appl1	195	14	2.5	2124	5	PCT-US92-05920-1	Sequence 1, Appl1
C 123	14	2.5	900	US-09-064-703-8	Sequence 8, Appl1	196	14	2.5	2144	2	US-08-525-742-9	Sequence 2, Appl1
C 124	14	2.5	915	US-08-394-152A-47	Sequence 9, Appl1	197	14	2.5	2173	1	US-08-036-210-6	Sequence 6, Appl1
C 125	14	2.5	930	US-08-913-842-14	Sequence 14, Appl1	198	14	2.5	2173	1	US-08-449-609-6	Sequence 6, Appl1
C 126	14	2.5	1017	5187262-7	Sequence 7, Appl1	199	14	2.5	2220	6	5171850-1	Sequence 7, Appl1
C 127	14	2.5	1018	US-08-913-842-14	Sequence 14, Appl1	200	14	2.5	2259	1	US-07-828-700-7	Sequence 1, Appl1
C 128	14	2.5	1035	US-08-417-210A-111	Sequence 111, App	201	14	2.5	2276	3	US-08-946-026-11	Sequence 28, Appl1
C 129	14	2.5	1042	US-08-765-381-3	Sequence 3, Appl1	202	14	2.5	2307	2	US-08-967-010-28	Sequence 28, Appl1
C 130	14	2.5	1070	US-08-441-597-1	Sequence 1, Appl1	203	14	2.5	2307	2	US-08-592-541-28	Sequence 28, Appl1
C 131	14	2.5	1079	US-08-765-381-1	Sequence 1, Appl1	204	14	2.5	2307	4	US-09-124-658-28	Sequence 28, Appl1
C 132	14	2.5	1096	US-09-056-153-1	Sequence 1, Appl1	205	14	2.5	2307	4	US-09-127-480-28	Sequence 28, Appl1
C 133	14	2.5	1102	5498499-1	Sequence 5, Appl1	206	14	2.5	2307	4	US-08-496-841C-28	Sequence 28, Appl1
C 134	14	2.5	1127	US-08-913-842-5	Sequence 5, Appl1	207	14	2.5	2309	2	US-08-036-210-10	Sequence 10, Appl1
C 135	14	2.5	1173	US-08-184-009-214	Sequence 214, App	208	14	2.5	2309	2	US-08-449-609-10	Sequence 10, Appl1
C 136	14	2.5	1173	US-08-458-356-214	Sequence 214, App	209	14	2.5	2441	1	US-08-920-812-12	Sequence 12, Appl1
C 137	14	2.5	1173	US-08-796-101-45	Sequence 45, Appl1	210	14	2.5	2441	1	US-08-920-812-12	Sequence 12, Appl1
C 138	14	2.5	1194	US-08-989-478-13	Sequence 13, Appl1	211	14	2.5	2441	1	US-08-921-177-12	Sequence 12, Appl1
C 139	14	2.5	1194	US-08-996-685-13	Sequence 13, Appl1	212	14	2.5	2441	1	US-08-362-577C-12	Sequence 12, Appl1
C 140	14	2.5	1235	5171685-1	Sequence 13, Appl1	213	14	2.5	2441	2	US-08-920-828-12	Sequence 12, Appl1
C 141	14	2.5	1236	518916-1	Sequence 13, Appl1	214	14	2.5	2539	2	US-08-432-016-1	Sequence 1, Appl1
C 142	14	2.5	1305	US-08-185-851A-1	Sequence 1, Appl1	215	14	2.5	2539	2	US-08-684-594-1	Sequence 1, Appl1
C 143	14	2.5	1337	US-08-467-023-1	Sequence 1, Appl1	216	14	2.5	2559	3	US-09-070-060-2	Sequence 2, Appl1
C 144	14	2.5	1349	US-08-676-782-10	Sequence 10, Appl1	217	14	2.5	2559	3	US-09-357-746-2	Sequence 2, Appl1
C 145	14	2.5	1353	US-08-611-280-1	Sequence 1, Appl1	218	14	2.5	2559	3	US-08-631-607-1	Sequence 1, Appl1
C 146	14	2.5	1368	US-08-204-288-1	Sequence 1, Appl1	219	14	2.5	2651	2	US-08-658-665-49	Sequence 49, Appl1
C 147	14	2.5	1387	US-08-525-742-3	Sequence 3, Appl1	220	14	2.5	2651	4	US-08-796-101-13	Sequence 13, Appl1
C 148	14	2.5	1505	US-08-909-965C-13	Sequence 13, Appl1	221	14	2.5	2692	2	US-08-036-210-14	Sequence 14, Appl1
C 149	14	2.5	1529	US-08-448-110-1	Sequence 1, Appl1	222	14	2.5	2780	1	US-08-441-139-1	Sequence 1, Appl1
C 150	14	2.5	1529	5436393-2	Sequence 1, Appl1	223	14	2.5	2852	3	US-09-027-137-2	Sequence 2, Appl1
C 151	14	2.5	1530	US-08-458-084-3	Sequence 3, Appl1	224	14	2.5	2852	3	US-08-458-434A-4	Sequence 4, Appl1
C 152	14	2.5	1530	US-08-205-508-3	Sequence 3, Appl1	225	14	2.5	2852	3	US-08-565-398-9	Sequence 9, Appl1
C 153	14	2.5	1530	US-08-482-148-8	Sequence 8, Appl1	226	14	2.5	2989	2	US-08-841-349-12	Sequence 12, Appl1
C 154	14	2.5	1530	PCT-US95-02944-8	Sequence 8, Appl1	227	14	2.5	3058	4	US-09-276-531-107	Sequence 107, App
C 155	14	2.5	1530	PCT-US95-02945-3	Sequence 3, Appl1	228	14	2.5	3065	2	US-08-209-521-28	Sequence 28, Appl1
C 156	14	2.5	1533	US-08-483-223-23	Sequence 23, Appl1	229	14	2.5	3087	1	US-08-849-480A-2	Sequence 2, Appl1
C 157	14	2.5	1533	US-08-485-938A-23	Sequence 23, Appl1	230	14	2.5	3298	2	US-08-208-008C-3	Sequence 3, Appl1
C 158	14	2.5	1533	US-08-910-041-23	Sequence 23, Appl1	231	14	2.5	3350	3	US-09-110-116-2	Sequence 2, Appl1
C 159	14	2.5	1533	US-09-328-474-23	Sequence 23, Appl1	232	14	2.5	3355	2	US-08-933-821-3	Sequence 3, Appl1
C 160	14	2.5	1533	US-09-100-546-23	Sequence 23, Appl1	233	14	2.5	3355	2	US-08-960-507-3	Sequence 3, Appl1
C 161	14	2.5	1533	US-09-010-715-23	Sequence 23, Appl1	234	14	2.5	3411	2	US-08-849-480A-1	Sequence 1, Appl1
C 162	14	2.5	1533	US-09-577-756-23	Sequence 23, Appl1	235	14	2.5	3539	1	US-08-796-101-11	Sequence 11, Appl1
C 163	14	2.5	1546	5514787-1	Sequence 23, Appl1	236	14	2.5	3539	1	US-08-485-568A-3	Sequence 3, Appl1
C 164	14	2.5	1567	US-09-276-531-75	Sequence 75, Appl1	237	14	2.5	3561	4	US-08-357-650-5	Sequence 5, Appl1
C 165	14	2.5	1590	US-09-064-703-1	Sequence 1, Appl1	238	14	2.5	3561	2	US-08-590-554A-3	Sequence 3, Appl1
C 166	14	2.5	1597	US-08-989-478-9	Sequence 9, Appl1	239	14	2.5	3561	2	US-09-184-223-3	Sequence 3, Appl1
C 167	14	2.5	1597	US-08-989-478-9	Sequence 9, Appl1	240	14	2.5	3561	2	PCT-US93-12682-5	Sequence 5, Appl1
C 168	14	2.5	1605	US-09-064-703-5	Sequence 5, Appl1	241	14	2.5	3592	3	US-08-714-918-63	Sequence 63, Appl1
C 169	14	2.5	1608	US-08-989-478-11	Sequence 11, Appl1	242	14	2.5	3592	4	US-09-265-315-63	Sequence 63, Appl1
C 170	14	2.5	1608	US-08-989-478-11	Sequence 11, Appl1	243	14	2.5	3592	4	US-09-265-315-63	Sequence 63, Appl1
C 171	14	2.5	1610	US-08-540-804-17	Sequence 17, Appl1	244	14	2.5	3891	1	US-08-480-604A-27	Sequence 27, Appl1
C 172	14	2.5	1610	US-08-218-265-17	Sequence 17, Appl1	245	14	2.5	3891	1	US-08-480-604A-27	Sequence 27, Appl1
C 173	14	2.5	1610	US-08-521-872-17	Sequence 17, Appl1	246	14	2.5	3891	1	US-08-480-604A-27	Sequence 27, Appl1

C 247	14	2.5	3891	2	US-08-405-496A-27	Sequence 27, Appl	C 320	13	2.3	20	1	US-08-409-442A-348	Sequence 348, App
C 248	14	2.5	3973	1	US-08-036-210-21	Sequence 21, Appl	C 321	13	2.3	20	2	US-08-469-609A-348	Sequence 348, App
C 249	14	2.5	3973	2	US-08-449-609-21	Sequence 21, Appl	C 322	13	2.3	20	3	US-09-289-267-59	Sequence 59, Appl
C 250	14	2.5	4071	4	US-09-091-117-3	Sequence 3, Appl1	C 323	13	2.3	20	4	US-09-143-190-348	Sequence 348, App
C 251	14	2.5	4144	1	US-08-218-686-1	Sequence 1, Appl1	C 324	13	2.3	20	4	US-09-359-756-45	Sequence 45, Appl
C 252	14	2.5	4144	3	US-08-460-242-1	Sequence 1, Appl1	C 325	13	2.3	22	4	US-08-882-046-91	Sequence 91, Appl
C 253	14	2.5	4184	2	US-08-785-310A-4	Sequence 4, Appl1	C 326	13	2.3	23	1	US-07-710-882-9	Sequence 9, Appl1
C 254	14	2.5	4319	2	PCT-US95-10661A-1	Sequence 1, Appl1	C 327	13	2.3	23	1	US-07-925-732-9	Sequence 9, Appl1
C 255	14	2.5	4427	2	US-08-658-665-48	Sequence 48, Appl	C 328	13	2.3	25	1	US-08-316-293-21	Sequence 21, Appl
C 256	14	2.5	4427	4	US-08-796-101-12	Sequence 12, Appl	C 329	13	2.3	25	1	US-08-071-601-14	Sequence 14, Appl
C 257	14	2.5	4450	4	US-08-617-8608-2	Sequence 2, Appl1	C 330	13	2.3	25	2	US-08-621-100-14	Sequence 14, Appl
C 258	14	2.5	4838	4	US-08-852-629-15	Sequence 15, Appl	C 331	13	2.3	25	4	US-09-047-347-6	Sequence 6, Appl1
C 259	14	2.5	4883	2	US-08-658-665-70	Sequence 70, Appl	C 332	13	2.3	30	1	US-08-073-799C-5	Sequence 5, Appl1
C 260	14	2.5	4893	4	US-08-796-101-34	Sequence 34, Appl	C 333	13	2.3	30	1	US-07-946-232-5	Sequence 5, Appl1
C 261	14	2.5	4972	4	US-09-035-648-17	Sequence 17, Appl	C 334	13	2.3	30	1	US-07-947-672-5	Sequence 5, Appl1
C 262	14	2.5	5062	2	US-08-658-665-187	Sequence 187, App	C 335	13	2.3	30	1	US-08-432-043-5	Sequence 5, Appl1
C 263	14	2.5	5062	4	US-08-796-101-42	Sequence 42, Appl	C 336	13	2.3	30	2	US-08-660-963-5	Sequence 5, Appl1
C 264	14	2.5	5173	1	US-08-242-677-1	Sequence 1, Appl1	C 337	13	2.3	30	2	US-08-629-001A-14	Sequence 14, Appl
C 265	14	2.5	5194	2	US-08-642-846-1	Sequence 1, Appl1	C 338	13	2.3	30	4	US-08-642-274D-220	Sequence 220, App
C 266	14	2.5	5224	2	US-08-874-186-46	Sequence 46, Appl	C 339	13	2.3	33	2	US-08-381-691-4	Sequence 4, Appl1
C 267	14	2.5	5324	2	US-09-070-060-1	Sequence 1, Appl1	C 340	13	2.3	34	2	US-08-793-410-15	Sequence 15, Appl
C 268	14	2.5	5372	2	US-09-357-746-1	Sequence 1, Appl1	C 341	13	2.3	44	6	5464756-29	Patent No. 5464756
C 269	14	2.5	5390	5	PCT-US96-12545-5	Sequence 5, Appl1	C 342	13	2.3	48	1	US-07-977-434-37	Sequence 37, Appl
C 270	14	2.5	5421	1	US-08-118-441-28	Sequence 28, Appl	C 343	13	2.3	48	1	US-08-458-819-37	Sequence 37, Appl
C 271	14	2.5	5421	3	US-08-338-579A-28	Sequence 28, Appl	C 344	13	2.3	48	5	PCT-US91-07035-37	Sequence 37, Appl
C 272	14	2.5	5421	5	PCT-US94-09851-28	Sequence 28, Appl	C 345	13	2.3	50	6	5240845-45	Patent No. 5240845
C 273	14	2.5	5529	3	US-08-869-696-1	Sequence 1, Appl1	C 346	13	2.3	51	1	US-08-409-442A-345	Sequence 345, App
C 274	14	2.5	5529	4	US-09-050-159-129	Sequence 129, App	C 347	13	2.3	51	2	US-08-469-609A-345	Sequence 345, App
C 275	14	2.5	5622	4	US-09-067-800-3	Sequence 3, Appl1	C 348	13	2.3	51	4	US-09-143-190-345	Sequence 345, App
C 276	14	2.5	5655	2	US-08-989-478-1	Sequence 1, Appl1	C 349	13	2.3	52	6	5240845-52	Patent No. 5240845
C 277	14	2.5	5655	3	US-08-996-685-1	Sequence 1, Appl1	C 350	13	2.3	98	1	US-07-710-882-12	Sequence 12, Appl
C 278	14	2.5	5655	3	US-08-880-179-2	Sequence 2, Appl1	C 351	13	2.3	98	1	US-07-910-882-13	Sequence 13, Appl
C 279	14	2.5	5715	4	US-09-107-847-1	Sequence 1, Appl1	C 352	13	2.3	98	1	US-07-925-732-12	Sequence 12, Appl
C 280	14	2.5	6169	2	US-08-875-154-2	Sequence 2, Appl1	C 353	13	2.3	98	1	US-07-925-732-13	Sequence 13, Appl
C 281	14	2.5	6659	4	US-09-212-971-5	Sequence 5, Appl1	C 354	13	2.3	108	2	US-08-418-085-8	Sequence 8, Appl1
C 282	14	2.5	6659	4	US-08-800-926A-5	Sequence 5, Appl1	C 355	13	2.3	108	4	US-09-099-011A-8	Sequence 8, Appl1
C 283	14	2.5	6702	4	US-08-987-439-2	Sequence 2, Appl1	C 356	13	2.3	122	4	US-08-454-557C-96	Sequence 96, Appl
C 284	14	2.5	6909	2	US-08-804-196-1	Sequence 1, Appl1	C 357	13	2.3	122	2	US-08-340-426B-96	Sequence 96, Appl
C 285	14	2.5	6909	2	US-08-658-340-1	Sequence 1, Appl1	C 358	13	2.3	132	2	US-08-450-673C-96	Sequence 96, Appl
C 286	14	2.5	6909	3	US-08-746-111-26	Sequence 26, Appl	C 359	13	2.3	132	5	PCT-US95-17111A-96	Sequence 96, Appl
C 287	14	2.5	7091	4	US-08-975-762-46	Sequence 46, Appl	C 360	13	2.3	133	6	5298404-2	Patent No. 5298404
C 288	14	2.5	7486	4	US-08-475-886-5	Sequence 5, Appl1	C 361	13	2.3	139	5	PCT-US93-06251-31	Sequence 31, Appl
C 289	14	2.5	7486	4	US-08-397-232-3	Sequence 3, Appl1	C 362	13	2.3	219	1	US-08-463-213-1	Sequence 1, Appl1
C 290	14	2.5	7488	4	US-08-475-886-3	Sequence 3, Appl1	C 363	13	2.3	219	6	5453566-1	Patent No. 5453566
C 291	14	2.5	7493	4	US-08-475-886-1	Sequence 1, Appl1	C 364	13	2.3	240	5	PCT-US95-10904-64	Sequence 64, Appl
C 292	14	2.5	7493	4	US-08-397-232-1	Sequence 1, Appl1	C 365	13	2.3	243	2	US-08-687-080-67	Sequence 67, Appl
C 293	14	2.5	7573	1	US-08-287-959-2	Sequence 2, Appl1	C 366	13	2.3	248	2	US-08-822-028-58	Sequence 58, Appl
C 294	14	2.5	7635	1	US-08-455-543A-23	Sequence 23, Appl	C 367	13	2.3	248	4	US-08-479-285-58	Sequence 58, Appl
C 295	14	2.5	7635	2	US-08-193-0788-29	Sequence 29, Appl	C 368	13	2.3	279	1	US-08-307-499-52	Sequence 52, Appl
C 296	14	2.5	7635	2	US-08-223-305C-23	Sequence 23, Appl	C 369	13	2.3	360	1	US-08-328-256-1	Sequence 1, Appl1
C 297	14	2.5	8920	2	US-08-446-855A-1	Sequence 1, Appl1	C 370	13	2.3	366	2	US-08-820-170A-2	Sequence 2, Appl1
C 298	14	2.5	8920	4	US-09-150-741-1	Sequence 1, Appl1	C 371	13	2.3	366	3	US-09-055-659-2	Sequence 2, Appl1
C 299	14	2.5	9100	2	US-08-743-637B-27	Sequence 27, Appl	C 372	13	2.3	366	4	US-09-273-565-2	Sequence 2, Appl1
C 300	14	2.5	9100	3	US-08-526-840B-27	Sequence 27, Appl	C 373	13	2.3	366	4	US-08-692-787-45	Sequence 45, Appl
C 301	14	2.5	9606	1	US-07-741-940-1	Sequence 1, Appl1	C 374	13	2.3	378	5	PCT-US94-04208-5	Sequence 5, Appl1
C 302	14	2.5	9606	1	US-08-289-548A-1	Sequence 1, Appl1	C 375	13	2.3	389	4	US-09-040-984-42	Sequence 42, Appl
C 303	14	2.5	9606	1	US-08-452-654-1	Sequence 1, Appl1	C 376	13	2.3	394	4	US-08-496-841C-46	Sequence 46, Appl
C 304	14	2.5	9606	2	US-08-370-235A-1	Sequence 1, Appl1	C 377	13	2.3	400	4	PCT-US94-04208-3	Sequence 3, Appl1
C 305	14	2.5	9919	3	US-08-880-179-1	Sequence 1, Appl1	C 378	13	2.3	400	2	PCT-US96-07329-1	Sequence 3, Appl1
C 306	14	2.5	10216	2	US-08-875-154-1	Sequence 1, Appl1	C 383	13	2.3	400	2	US-08-592-541-46	Sequence 46, Appl
C 307	14	2.5	10409	3	US-08-772-440-33	Sequence 33, Appl	C 384	13	2.3	400	4	US-09-124-698-46	Sequence 46, Appl
C 308	14	2.5	10917	2	US-08-926-842B-11	Sequence 11, Appl	C 380	13	2.3	400	4	US-09-127-480-46	Sequence 46, Appl
C 309	14	2.5	12537	2	US-08-611-280-4	Sequence 4, Appl1	C 381	13	2.3	404	5	US-08-496-841C-46	Sequence 46, Appl
C 310	14	2.5	12687	3	US-08-676-169-1	Sequence 1, Appl1	C 382	13	2.3	404	5	PCT-US94-04208-3	Sequence 3, Appl1
C 311	14	2.5	12687	3	US-08-981-459-1	Sequence 1, Appl1	C 383	13	2.3	404	5	PCT-US96-07329-1	Sequence 3, Appl1
C 312	14	2.5	14855	2	US-08-687-080-59	Sequence 59, Appl	C 384	13	2.3	404	5	PCT-US93-01676A-5	Sequence 5, Appl1
C 313	14	2.5	15144	3	US-08-458-434A-6	Sequence 6, Appl1	C 385	13	2.3	466	1	US-08-324-243-36	Sequence 36, Appl
C 314	14	2.5	16442	3	US-08-781-891-208	Sequence 208, App	C 386	13	2.3	466	1	US-08-532-590-36	Sequence 36, Appl
C 315	14	2.5	35100	2	US-08-770-379-17	Sequence 17, Appl	C 387	13	2.3	466	4	US-08-717-294-36	Sequence 36, Appl
C 316	14	2.5	35100	4	US-08-757-669A-17	Sequence 17, Appl	C 388	13	2.3	466	5	PCT-US95-11511-36	Sequence 36, Appl
C 317	14	2.5	51952	4	US-08-947-823-1	Sequence 1, Appl1	C 389	13	2.3	489	6	5464756-19	Patent No. 5464756
C 318	14	2.5	87350	4	US-08-781-891-79	Sequence 79, Appl	C 390	13	2.3	503	6	5464756-19	Patent No. 5464756
C 319	13	2.3	18	2	US-09-156-424-36	Sequence 36, Appl	C 391	13	2.3	503	1	US-08-123-943A-15	Sequence 15, Appl
							C 392	13	2.3	506	1	US-08-111-316-1	Sequence 1, Appl1

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394	13	2.3	537	5	PCT-US95-10904-70	Sequence 70, Appl	C 467	13	2.3	992	2	US-08-374-843B-9	Sequence 9, Appl1
395	13	2.3	540	1	US-08-117-080-15	Sequence 15, Appl	C 468	13	2.3	992	1	US-08-905-420-9	Sequence 9, Appl1
C 396	13	2.3	543	1	US-07-912-900-25	Sequence 25, Appl	C 469	13	2.3	993	1	US-08-364-081-2	Sequence 2, Appl1
C 398	13	2.3	543	2	US-08-285-309-25	Sequence 25, Appl	C 470	13	2.3	993	1	US-08-630-581-2	Sequence 2, Appl1
C 399	13	2.3	543	2	US-08-502-046-25	Sequence 25, Appl	C 471	13	2.3	993	5	PCT-US95-1658-2	Sequence 2, Appl1
C 400	13	2.3	547	1	US-08-313-075A-31	Sequence 31, Appl	C 472	13	2.3	997	1	US-08-374-843B-16	Sequence 16, Appl
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402	13	2.3	573	5	PCT-US95-07289-13	Sequence 13, Appl	C 474	13	2.3	1001	2	US-08-982-956-2	Sequence 2, Appl1
403	13	2.3	573	1	US-08-319-590-24	Sequence 24, Appl	C 475	13	2.3	1001	4	US-09-228-317-2	Sequence 2, Appl1
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406	13	2.3	573	2	US-09-005-069-24	Sequence 24, Appl	C 478	13	2.3	1022	1	US-08-960-780-33	Sequence 33, Appl1
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408	13	2.3	591	2	US-08-630-822A-34	Sequence 34, Appl	C 480	13	2.3	1025	3	US-08-480-640A-224	Sequence 224, App
409	13	2.3	591	2	US-09-005-069-34	Sequence 34, Appl	C 481	13	2.3	1062	2	US-08-671-978A-1	Sequence 1, Appl1
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411	13	2.3	601	3	US-09-080-855-34	Sequence 34, Appl	C 483	13	2.3	1070	4	US-09-118-442-16	Sequence 16, Appl
412	13	2.3	619	3	US-08-714-918-98	Sequence 98, Appl	C 484	13	2.3	1074	2	US-09-156-428-1	Sequence 1, Appl1
413	13	2.3	619	4	US-09-265-315-98	Sequence 98, Appl	C 485	13	2.3	1079	1	US-08-454-196-16	Sequence 16, Appl
414	13	2.3	619	4	US-09-265-315-98	Sequence 98, Appl	C 486	13	2.3	1079	3	US-09-064-033-16	Sequence 28, Appl
415	13	2.3	648	2	US-08-935-396-9	Sequence 9, Appl1	C 487	13	2.3	1082	4	US-09-118-442-28	Sequence 30, Appl
416	13	2.3	668	2	US-09-413-452-6	Sequence 6, Appl1	C 488	13	2.3	1083	4	US-09-276-531-30	Sequence 30, Appl
417	13	2.3	667	3	US-08-845-546-9	Sequence 9, Appl1	C 489	13	2.3	1097	4	US-09-094-103-5	Sequence 5, Appl1
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C 421	13	2.3	730	1	US-08-036-555B-147	Sequence 147, App	C 493	13	2.3	1116	3	US-09-345-603-3	Sequence 3, Appl1
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C 430	13	2.3	730	4	US-08-734-664A-147	Sequence 147, App	C 502	13	2.3	1158	1	US-08-891-258-4	Sequence 4, Appl1
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C 432	13	2.3	804	5	PCT-US95-06846A-147	Sequence 147, App	C 504	13	2.3	1158	5	PCT-US93-06243-4	Sequence 4, Appl1
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436	13	2.3	816	2	US-08-822-028-26	Sequence 26, Appl	C 508	13	2.3	1169	4	US-08-307-591-2	Sequence 2, Appl
437	13	2.3	816	4	US-08-479-285-25	Sequence 25, Appl	C 509	13	2.3	1199	4	US-09-080-963-1	Sequence 1, Appl1
438	13	2.3	819	2	US-08-822-028-25	Sequence 25, Appl	C 510	13	2.3	1200	1	US-08-040-548-32	Sequence 32, Appl
439	13	2.3	819	4	US-08-479-285-25	Sequence 25, Appl	C 511	13	2.3	1200	1	US-08-466-344-32	Sequence 32, Appl
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442	13	2.3	839	1	US-08-474-633A-93	Sequence 93, Appl	C 514	13	2.3	1209	2	US-08-200-724A-4	Sequence 4, Appl1
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C 446	13	2.3	842	3	US-09-055-699-3	Sequence 3, Appl1	C 518	13	2.3	1221	4	US-09-286-691-13	Sequence 13, Appl
C 447	13	2.3	842	4	US-09-273-565-3	Sequence 3, Appl1	C 519	13	2.3	1242	4	US-09-147-928-1	Sequence 1, Appl1
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450	13	2.3	860	4	US-08-975-762-31	Sequence 31, Appl	C 522	13	2.3	1257	1	US-07-946-232-7	Sequence 7, Appl1
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C 457	13	2.3	917	1	US-07-949-812-1	Sequence 1, Appl1	C 529	13	2.3	1272	2	US-08-660-963-7	Sequence 7, Appl1
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541	13	2.3	1368	4	US-08-972-927-8	Sequence 8, App11	c 614	13	2.3	1764	5	PCR-US95-0686A-150	Sequence 150, App
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577	13	2.3	1601	6	5447867-2	Patent No. 5447867	c 650	13	2.3	2060	4	US-09-205-143-1	Sequence 1, App11
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582	13	2.3	1678	1	US-08-384-556A-6	Sequence 6, App11	c 655	13	2.3	2075	3	US-08-750-391-7	Sequence 7, App11
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584	13	2.3	1678	5	PCR-US94-12364-10	Sequence 10, App1	c 657	13	2.3	2081	5	PCR-US91-01750-3	Sequence 3, App11
585	13	2.3	1678	5	PCR-US95-07753-6	Sequence 6, App11	c 658	13	2.3	2085	2	US-08-283-917-8	Sequence 8, App11
586	13	2.3	1680	2	US-08-700-152A-3	Sequence 3, App11	c 659	13	2.3	2085	2	US-08-961-716-8	Sequence 8, App11
587	13	2.3	1690	2	US-08-461-812-3	Sequence 3, App11	c 660	13	2.3	2097	2	US-08-655-345-3	Sequence 3, App11
588	13	2.3	1713	2	US-08-467-948A-1	Sequence 1, App11	c 661	13	2.3	2097	3	US-09-183-275-3	Sequence 3, App11
589	13	2.3	1713	2	US-08-467-948A-1	Sequence 1, App11	c 662	13	2.3	2097	5	PCR-US96-08407-3	Sequence 3, App11
590	13	2.3	1743	3	US-08-482-677-9	Sequence 9, App11	c 663	13	2.3	2106	1	US-07-718-535-4	Sequence 4, App11
591	13	2.3	1750	3	US-08-415-823-1	Sequence 1, App11	c 664	13	2.3	2106	1	US-08-161-999-4	Sequence 1, App11
592	13	2.3	1750	2	US-09-086-662-1	Sequence 1, App11	c 665	13	2.3	2116	3	US-08-845-546-11	Sequence 11, App1
593	13	2.3	1755	2	US-08-307-588-3	Sequence 3, App11	c 666	13	2.3	2115	3	US-09-078-862-1	Sequence 1, App11
594	13	2.3	1758	5	PCR-US92-01015-1	Sequence 1, App11	c 667	13	2.3	2145	3	US-08-285-641-19	Sequence 19, App1
595	13	2.3	1760	3	US-09-150-133-8	Sequence 8, App11	c 668	13	2.3	2157	1	US-08-451-715A-30	Sequence 30, App1
596	13	2.3	1760	3	US-09-150-141-8	Sequence 8, App11	c 669	13	2.3	2166	2	US-08-408-095-30	Sequence 30, App1
597	13	2.3	1760	4	US-09-374-493-8	Sequence 8, App11	c 670	13	2.3	2178	3	US-08-781-891-72	Sequence 72, App1
598	13	2.3	1760	4	US-09-374-493-8	Sequence 8, App11	c 671	13	2.3	2191	1	US-08-318-905-22	Sequence 22, App1
599	13	2.3	1760	4	US-09-374-493-8	Sequence 8, App11	c 672	13	2.3	2191	1	US-08-483-232-22	Sequence 22, App1
600	13	2.3	1761	4	US-08-481-190-1	Sequence 1, App11	c 673	13	2.3	2191	1	US-08-483-140-22	Sequence 22, App1
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603	13	2.3	1764	1	US-08-036-555B-150	Sequence 150, App	c 676	13	2.3	2191	3	US-09-328-474-22	Sequence 22, App1
604	13	2.3	1764	1	US-08-469-569-150	Sequence 150, App	c 677	13	2.3	2191	3	US-09-100-546-22	Sequence 22, App1
605	13	2.3	1764	1	US-08-249-322A-150	Sequence 150, App	c 678	13	2.3	2191	4	US-09-010-715-22	Sequence 22, App1
606	13	2.3	1764	1	US-08-469-526A-150	Sequence 150, App	c 679	13	2.3	2191	4	US-09-577-715-22	Sequence 22, App1
607	13	2.3	1764	2	US-08-734-591A-150	Sequence 150, App	c 680	13	2.3	2192	3	US-09-289-267-1	Sequence 1, App11
608	13	2.3	1764	2	US-08-469-660-150	Sequence 150, App	c 681	13	2.3	2208	3	US-08-539-205A-1	Sequence 1, App11
609	13	2.3	1764	3	US-08-341-018-57	Sequence 57, App1	c 682	13	2.3	2222	3	US-09-197-380-1	Sequence 1, App11
610	13	2.3	1764	3	US-08-470-335-150	Sequence 150, App	c 683	13	2.3	2255	3	US-08-714-918-105	Sequence 105, App
611	13	2.3	1764	4	US-08-733-021-150	Sequence 150, App	c 684	13	2.3	2255	4	US-09-265-315-105	Sequence 105, App

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C 686	13	2.3	2264	3	US-08-262-220-5	Sequence 5, Appl1	C 759	13	2.3	2657	1	US-07-718-535-2	Sequence 2, Appl1
C 687	13	2.3	2264	3	US-08-471-733-5	Sequence 5, Appl1	C 760	13	2.3	2657	1	US-08-161-999-2	Sequence 2, Appl1
C 688	13	2.3	2264	3	US-08-468-878-5	Sequence 5, Appl1	C 761	13	2.3	2667	2	US-08-286-819A-17	Sequence 17, Appl
C 689	13	2.3	2264	4	US-08-750-494-5	Sequence 5, Appl1	C 762	13	2.3	2667	2	US-08-980-357-17	Sequence 17, Appl
C 690	13	2.3	2268	4	US-09-050-159-133	Sequence 133, App	C 763	13	2.3	2734	6	5304637-26	Patent No. 5304637
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C 692	13	2.3	2273	4	US-09-265-315-40	Sequence 40, Appl	C 765	13	2.3	2748	6	5304637-25	Sequence 17, Appl
C 693	13	2.3	2273	4	US-09-265-315-40	Sequence 40, Appl	C 766	13	2.3	2760	1	US-08-026-138E-18	Sequence 18, Appl
C 694	13	2.3	2277	1	US-08-496-855A-1	Sequence 1, Appl1	C 767	13	2.3	2760	1	US-08-026-138E-19	Sequence 19, Appl
C 695	13	2.3	2306	1	US-08-378-698-3	Sequence 3, Appl1	C 768	13	2.3	2760	4	US-09-198-484-1	Sequence 1, Appl1
C 696	13	2.3	2306	5	PCT-US96-00728-3	Sequence 3, Appl1	C 769	13	2.3	2764	4	US-08-471-454-1	Sequence 1, Appl1
C 697	13	2.3	2310	4	US-08-956-182-13	Sequence 13, Appl	C 770	13	2.3	2784	2	US-08-466-974-1	Sequence 1, Appl1
C 698	13	2.3	2322	1	US-08-618-164-1	Sequence 1, Appl1	C 771	13	2.3	2784	2	US-08-471-453-1	Sequence 1, Appl1
C 699	13	2.3	2327	4	US-09-157-077-1	Sequence 1, Appl1	C 772	13	2.3	2796	1	US-08-261-677-8	Sequence 8, Appl1
C 700	13	2.3	2367	1	US-08-441-139-3	Sequence 3, Appl1	C 773	13	2.3	2796	1	US-08-384-556A-8	Sequence 4, Appl1
C 701	13	2.3	2404	1	US-08-311-023-3	Sequence 3, Appl1	C 774	13	2.3	2796	2	US-08-331-355A-8	Sequence 8, Appl1
C 702	13	2.3	2423	3	US-08-714-918-86	Sequence 86, Appl	C 775	13	2.3	2796	2	US-08-777-147-5	Sequence 5, Appl1
C 703	13	2.3	2423	4	US-09-265-315-86	Sequence 86, Appl	C 776	13	2.3	2796	4	PCT-US94-12364-8	Sequence 8, Appl1
C 704	13	2.3	2423	4	US-09-265-315-86	Sequence 86, Appl	C 777	13	2.3	2796	5	PCT-US94-12364-8	Sequence 8, Appl1
C 705	13	2.3	2433	1	US-08-248-021A-1	Sequence 1, Appl1	C 778	13	2.3	2796	5	PCT-US95-07753-4	Sequence 4, Appl1
C 706	13	2.3	2434	3	US-08-793-331-3	Sequence 3, Appl1	C 779	13	2.3	2800	2	US-08-874-138-1	Sequence 1, Appl1
C 707	13	2.3	2436	1	US-08-306-691B-16	Sequence 16, Appl	C 780	13	2.3	2800	2	US-08-874-138-5	Sequence 5, Appl1
C 708	13	2.3	2443	2	US-08-745-934-2	Sequence 2, Appl1	C 781	13	2.3	2814	2	US-08-743-637B-186	Sequence 186, App
C 709	13	2.3	2456	2	US-08-813-150-3	Sequence 3, Appl1	C 782	13	2.3	2823	1	US-08-398-008A-1	Sequence 1, Appl1
C 710	13	2.3	2475	2	US-08-655-345-1	Sequence 1, Appl1	C 783	13	2.3	2823	2	US-08-893-333-1	Sequence 8, Appl1
C 711	13	2.3	2475	2	US-09-183-275-1	Sequence 1, Appl1	C 784	13	2.3	2834	1	US-08-276-151-8	Sequence 1, Appl1
C 712	13	2.3	2475	5	PCT-US96-08407-1	Sequence 1, Appl1	C 785	13	2.3	2837	4	US-09-156-316-11	Sequence 11, Appl
C 713	13	2.3	2494	4	US-08-714-918-3	Sequence 3, Appl1	C 786	13	2.3	2861	1	US-08-299-953-1	Sequence 1, Appl1
C 714	13	2.3	2494	4	US-09-265-315-3	Sequence 3, Appl1	C 787	13	2.3	2861	1	US-08-459-415-1	Sequence 1, Appl1
C 715	13	2.3	2494	4	US-09-265-315-3	Sequence 3, Appl1	C 788	13	2.3	2861	5	PCT-US95-11331-1	Sequence 1, Appl1
C 716	13	2.3	2498	1	US-07-943-843-3	Sequence 3, Appl1	C 789	13	2.3	2862	1	US-08-148-209A-1	Sequence 1, Appl1
C 717	13	2.3	2498	1	US-08-347-003-3	Sequence 3, Appl1	C 790	13	2.3	2875	4	US-08-714-918-8	Sequence 8, Appl1
C 718	13	2.3	2511	1	US-08-363-560-1	Sequence 1, Appl1	C 791	13	2.3	2875	4	US-09-265-315-8	Sequence 8, Appl1
C 719	13	2.3	2515	3	US-08-714-918-37	Sequence 37, Appl	C 792	13	2.3	2887	5	US-09-265-315-8	Sequence 8, Appl1
C 720	13	2.3	2515	4	US-09-265-315-37	Sequence 37, Appl	C 793	13	2.3	2887	5	PCT-US96-10521-14	Sequence 14, Appl
C 721	13	2.3	2521	4	US-09-265-315-37	Sequence 37, Appl	C 794	13	2.3	2915	2	US-08-500-837A-1	Sequence 1, Appl1
C 722	13	2.3	2521	1	US-08-186-228-59	Sequence 59, Appl	C 795	13	2.3	2926	2	US-08-724-394A-13	Sequence 13, Appl
C 723	13	2.3	2521	1	US-08-332-643-53	Sequence 53, Appl	C 796	13	2.3	2940	3	US-08-689-421-78	Sequence 28, Appl
C 724	13	2.3	2521	1	US-08-332-638-59	Sequence 59, Appl	C 797	13	2.3	2940	4	US-09-389-528-28	Sequence 28, Appl
C 725	13	2.3	2524	1	US-08-317-522A-1	Sequence 1, Appl1	C 798	13	2.3	2968	3	US-09-022-659-1	Sequence 1, Appl1
C 726	13	2.3	2524	1	US-08-439-818A-1	Sequence 1, Appl1	C 799	13	2.3	2971	1	US-07-718-575-7	Sequence 7, Appl1
C 727	13	2.3	2524	2	US-08-751-965-1	Sequence 1, Appl1	C 800	13	2.3	2971	1	US-08-481-206-7	Sequence 7, Appl1
C 728	13	2.3	2524	2	US-08-738-975-1	Sequence 1, Appl1	C 801	13	2.3	2971	2	US-08-486-269A-7	Sequence 7, Appl1
C 729	13	2.3	2524	2	US-08-728-626-1	Sequence 1, Appl1	C 802	13	2.3	2991	1	US-08-795-430-48	Sequence 48, Appl
C 730	13	2.3	2524	4	US-08-808-599A-1	Sequence 1, Appl1	C 803	13	2.3	3003	1	US-08-434-730-15	Sequence 15, Appl
C 731	13	2.3	2558	1	US-08-477-476-1	Sequence 1, Appl1	C 804	13	2.3	3012	1	US-08-453-742-1	Sequence 1, Appl1
C 732	13	2.3	2558	2	US-08-993-210-1	Sequence 1, Appl1	C 805	13	2.3	3012	1	US-08-454-464-1	Sequence 1, Appl1
C 733	13	2.3	2558	5	PCT-US96-07354-1	Sequence 1, Appl1	C 806	13	2.3	3012	1	US-08-453-222-1	Sequence 1, Appl1
C 734	13	2.3	2570	2	US-09-056-075-2	Sequence 2, Appl1	C 807	13	2.3	3012	1	US-08-453-802-1	Sequence 1, Appl1
C 735	13	2.3	2601	4	US-09-039-773A-2	Sequence 2, Appl1	C 808	13	2.3	3012	2	US-08-475-427-5	Sequence 5, Appl1
C 736	13	2.3	2606	2	US-08-701-233B-1	Sequence 1, Appl1	C 809	13	2.3	3012	2	US-07-842-165-5	Sequence 5, Appl1
C 737	13	2.3	2607	2	US-08-743-637B-170	Sequence 170, App	C 810	13	2.3	3014	2	US-09-429-093-1	Sequence 1, Appl1
C 738	13	2.3	2607	3	US-08-526-840B-170	Sequence 170, App	C 811	13	2.3	3018	4	US-08-942-572-1	Sequence 1, Appl1
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C 740	13	2.3	2622	1	US-08-766-014-23	Sequence 23, Appl	C 813	13	2.3	3027	2	US-09-282-803B-9	Sequence 9, Appl1
C 741	13	2.3	2631	1	US-08-717-515-3	Sequence 3, Appl1	C 814	13	2.3	3033	1	US-08-482-037A-1	Sequence 1, Appl1
C 742	13	2.3	2631	1	US-08-785-071A-1	Sequence 1, Appl1	C 815	13	2.3	3055	1	US-08-236-754-1	Sequence 1, Appl1
C 743	13	2.3	2631	3	US-09-012-872-1	Sequence 1, Appl1	C 816	13	2.3	3077	5	US-08-074-121-1	Sequence 1, Appl1
C 744	13	2.3	2631	3	US-08-253-785-1	Sequence 1, Appl1	C 817	13	2.3	3077	5	PCT-US94-06447-1	Sequence 1, Appl1
C 745	13	2.3	2645	4	US-08-960-780-31	Sequence 31, Appl	C 818	13	2.3	3084	1	US-08-551-437-1	Sequence 1, Appl1
C 746	13	2.3	2649	2	US-08-718-964-1	Sequence 1, Appl1	C 819	13	2.3	3126	4	US-09-004-225-1	Sequence 1, Appl1
C 747	13	2.3	2649	2	US-09-039-964A-1	Sequence 1, Appl1	C 820	13	2.3	3172	4	US-08-929-329-2	Sequence 2, Appl1
C 748	13	2.3	2651	1	US-08-842-341-1	Sequence 1, Appl1	C 821	13	2.3	3172	1	US-07-741-940-3	Sequence 3, Appl1
C 749	13	2.3	2651	1	US-08-462-949-1	Sequence 1, Appl1	C 822	13	2.3	3172	1	US-08-289-548A-3	Sequence 3, Appl1
C 750	13	2.3	2651	2	US-08-023-764B-1	Sequence 1, Appl1	C 823	13	2.3	3172	1	US-08-452-654-3	Sequence 3, Appl1
C 751	13	2.3	2653	2	US-08-589-711-1	Sequence 1, Appl1	C 824	13	2.3	3172	4	US-08-452-655B-3	Sequence 3, Appl1
C 752	13	2.3	2655	1	US-08-471-033-4	Sequence 4, Appl1	C 825	13	2.3	3172	4	US-08-450-382-3	Sequence 3, Appl1
C 753	13	2.3	2655	2	US-08-471-044-4	Sequence 4, Appl1	C 826	13	2.3	3237	2	US-08-419-075-26	Sequence 26, Appl
C 754	13	2.3	2655	2	US-08-463-483A-4	Sequence 4, Appl1	C 827	13	2.3	3244	2	US-08-321-670-1	Sequence 1, Appl1
C 755	13	2.3	2655	2	US-08-471-046A-4	Sequence 4, Appl1	C 828	13	2.3	3250	4	US-08-617-860B-1	Sequence 1, Appl1
C 756	13	2.3	2655	2	US-08-470-566B-4	Sequence 4, Appl1	C 829	13	2.3	3260	1	US-08-049-254-1	Sequence 1, Appl1
C 757	13	2.3	2655	2	US-08-469-334-4	Sequence 4, Appl1	C 830	13	2.3	3260	1	US-08-472-934-1	Sequence 1, Appl1



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832	13	2.3	3260	2	US-08-461-146C-1	Sequence 1, App11	c 905	13	2.3	3872	2	US-08-331-081B-4	Sequence 4, App11
833	13	2.3	3260	3	US-08-461-145C-1	Sequence 1, App11	906	13	2.3	3878	4	US-08-651-472-65	Sequence 65, App1
c 834	13	2.3	3279	4	US-08-851-843A-1	Sequence 109, App	907	13	2.3	3881	1	US-08-299-953-2	Sequence 2, App11
c 835	13	2.3	3279	4	US-08-974-549A-109	Sequence 8, App11	908	13	2.3	3881	1	US-08-459-415-2	Sequence 2, App11
836	13	2.3	3287	1	US-08-920-821-8	Sequence 8, App11	909	13	2.3	3881	5	PCT-US85-11231-2	Sequence 2, App11
837	13	2.3	3287	1	US-08-920-827-8	Sequence 8, App11	910	13	2.3	3901	1	US-08-326-297-1	Sequence 1, App11
838	13	2.3	3287	1	US-08-921-177-8	Sequence 8, App11	911	13	2.3	3901	1	US-08-617-454-1	Sequence 1, App11
839	13	2.3	3287	1	US-08-362-577C-8	Sequence 8, App11	912	13	2.3	3901	5	PCT-US94-01144-1	Sequence 1, App11
840	13	2.3	3287	2	US-08-920-828-8	Sequence 8, App11	913	13	2.3	3926	2	US-08-731-722-1	Sequence 1, App11
c 841	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	914	13	2.3	3926	2	US-08-731-722-2	Sequence 2, App11
c 842	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	915	13	2.3	3933	2	US-08-731-722-3	Sequence 2, App11
c 843	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 916	13	2.3	3943	2	US-08-369-796-3	Sequence 3, App11
c 844	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 917	13	2.3	3943	2	US-08-852-091-3	Sequence 3, App11
c 845	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 918	13	2.3	3943	2	US-08-852-091-3	Sequence 3, App11
c 846	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 919	13	2.3	3943	2	US-08-820-754-3	Sequence 3, App11
c 847	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 920	13	2.3	3943	3	US-08-956-652-3	Sequence 3, App11
c 848	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 921	13	2.3	3943	3	US-08-956-652-3	Sequence 3, App11
c 849	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 922	13	2.3	3943	4	US-08-948-547-3	Sequence 3, App11
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851	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 924	13	2.3	3943	4	US-08-602-093-6	Sequence 3, App11
852	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 925	13	2.3	3981	1	US-08-259-164-1	Sequence 1, App11
853	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 926	13	2.3	4000	2	US-08-861-464-5	Sequence 5, App11
854	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 927	13	2.3	4000	2	US-08-396-001-5	Sequence 5, App11
c 855	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 928	13	2.3	4003	4	US-09-087-465-1	Sequence 1, App11
c 856	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 929	13	2.3	4010	5	PCT-US94-07297-40	Sequence 1, App11
c 857	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 930	13	2.3	4020	5	PCT-US91-02560-1	Sequence 1, App11
c 858	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 931	13	2.3	4041	2	US-08-471-033-22	Sequence 22, App1
c 859	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 932	13	2.3	4041	2	US-08-471-033-22	Sequence 22, App1
c 860	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 933	13	2.3	4041	2	US-08-471-033-22	Sequence 22, App1
c 861	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 934	13	2.3	4041	2	US-08-471-033-22	Sequence 22, App1
c 862	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 935	13	2.3	4041	2	US-08-470-566B-22	Sequence 22, App1
c 863	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 936	13	2.3	4041	2	US-08-469-334-22	Sequence 22, App1
c 864	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 937	13	2.3	4041	1	US-09-300-529-22	Sequence 22, App1
865	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 938	13	2.3	4044	2	US-08-271-354-5	Sequence 5, App11
c 866	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 939	13	2.3	4044	2	US-08-565-861-5	Sequence 5, App11
c 867	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 940	13	2.3	4044	5	PCT-US94-07658-5	Sequence 5, App11
c 868	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 941	13	2.3	4074	4	US-08-471-033-19	Sequence 19, App1
c 869	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 942	13	2.3	4074	2	US-08-471-044-19	Sequence 19, App1
c 870	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 943	13	2.3	4074	2	US-08-463-483A-19	Sequence 19, App1
c 871	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 944	13	2.3	4074	2	US-08-471-046A-19	Sequence 19, App1
c 872	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 945	13	2.3	4074	2	US-08-470-566B-22	Sequence 22, App1
c 873	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 946	13	2.3	4074	2	US-08-469-334-19	Sequence 19, App1
c 874	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 947	13	2.3	4074	3	US-09-300-529-19	Sequence 19, App1
c 875	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 948	13	2.3	4094	1	US-08-571-758-5	Sequence 5, App11
c 876	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 949	13	2.3	4094	1	US-08-909-984A-5	Sequence 5, App11
c 877	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 950	13	2.3	4094	1	US-08-909-984-5	Sequence 5, App11
c 878	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 951	13	2.3	4118	1	US-08-119-125A-3	Sequence 3, App11
c 879	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 952	13	2.3	4145	4	US-08-651-472-62	Sequence 62, App1
c 880	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 953	13	2.3	4203	2	US-08-866-757-1	Sequence 1, App11
c 881	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 954	13	2.3	4245	2	US-09-153-593-1	Sequence 1, App11
c 882	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 955	13	2.3	4245	2	US-08-929-967-4	Sequence 4, App11
c 883	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 956	13	2.3	4277	2	US-08-651-472-63	Sequence 63, App1
c 884	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 957	13	2.3	4291	2	US-08-651-472-63	Sequence 63, App1
c 885	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 958	13	2.3	4296	4	US-08-417-210A-81	Sequence 81, App1
c 886	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 959	13	2.3	4296	4	US-09-060-410-3	Sequence 3, App11
c 887	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 960	13	2.3	4328	1	US-08-322-742-12	Sequence 12, App1
c 888	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 961	13	2.3	4359	3	US-08-331-625A-1	Sequence 1, App11
c 889	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 962	13	2.3	4359	5	PCT-US93-04384-17	Sequence 17, App1
c 890	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 963	13	2.3	4359	5	PCT-US93-04697-1	Sequence 1, App11
c 891	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 964	13	2.3	4362	2	US-08-455-073A-1	Sequence 1, App11
c 892	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 965	13	2.3	4407	2	US-08-455-073A-1	Sequence 1, App11
c 893	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 966	13	2.3	4407	2	PCT-US93-05701-1	Sequence 1, App11
c 894	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 967	13	2.3	4411	2	US-08-929-967-5	Sequence 5, App11
c 895	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 968	13	2.3	4411	2	US-08-929-967-5	Sequence 5, App11
c 896	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 969	13	2.3	4411	2	US-08-929-967-5	Sequence 5, App11
c 897	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 970	13	2.3	4411	2	US-08-929-967-5	Sequence 5, App11
c 898	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 971	13	2.3	4411	2	US-08-929-967-5	Sequence 5, App11
c 899	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 972	13	2.3	4411	2	US-08-929-967-5	Sequence 5, App11
c 900	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 973	13	2.3	4411	2	US-08-929-967-5	Sequence 5, App11
c 901	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 974	13	2.3	4411	2	US-08-929-967-5	Sequence 5, App11
c 902	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 975	13	2.3	4411	2	US-08-929-967-5	Sequence 5, App11
903	13	2.3	3287	2	US-08-453-742-26	Sequence 26, App1	c 976	13	2.3	4411	2	US-08-929-967-5	Sequence 5, App11



ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,359A  
FILING DATE: February 16, 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: HAILE, LISA A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 09010/010001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 NUCLEOTIDES  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: CDNA  
US-08-602-359A-2

Query Match 3 8%; Score 21; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 0.095;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 535 AATCATACACTAAGCATAG 555  
|||||  
DB 31 AATCATACACTAAGCATAG 11

RESULT 3  
US-08-602-359A-1  
Sequence 1, Application US/08602359A  
Patent No. 5942430  
GENERAL INFORMATION:  
APPLICANT: ROBERTSON, Daniel E.  
APPLICANT: MURPHY, Dennis  
APPLICANT: REID, John  
APPLICANT: MAFFIA, Anthony  
APPLICANT: LINK, Steven  
APPLICANT: SWANSON, Ronald V.  
APPLICANT: WARREN, Patrick V.  
APPLICANT: KOSMOTKA, Anna  
TITLE OF INVENTION: ESTERASES  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & RICHARDSON P.C.  
STREET: 4225 EXECUTIVE SQUARE, STE 1400  
CITY: LA JOLLA  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,359A  
FILING DATE: February 16, 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: HAILE, LISA A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 09010/010001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 52 NUCLEOTIDES  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: CDNA  
US-08-602-359A-1

Query Match 3 8%; Score 21; DB 2; Length 52;  
Best Local Similarity 100.0%; Pred. No. 0.095;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTTTAAACAAGCACTCT 21  
|||||  
DB 32 ATGCTTTAAACAAGCACTCT 52

RESULT 4  
US-08-781-891-207/C  
Sequence 207, Application US/08781891  
Patent No. 6090620  
GENERAL INFORMATION:  
APPLICANT: Fu, Ying-Hui  
APPLICANT: Yu, Chang-En  
APPLICANT: Oshima, Junko  
APPLICANT: Mulligan, John T.  
APPLICANT: Schellenberg, Gerald D.  
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO  
NUMBER OF SEQUENCES: 209  
TITLE OF INVENTION: WERNER'S SYNDROME  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781,891  
FILING DATE: 27-DEC-1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6090620tenburg Ph.D., Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 240052,419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 207:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29604 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-781-891-207

Query Match 3 2%; Score 18; DB 3; Length 29604;  
Best Local Similarity 100.0%; Pred. No. 3;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 99 ATGCTTAATATATGCAA 116  
|||||

Db 29176 ATGCTTAATATATGCAA 29159

RESULT 5  
5256558-7/c  
PATENT NO. 5256558  
APPLICANT: CORUZZI, GLORIA M.; TSAI, FONG-YING  
TITLE OF INVENTION: GENE ENCODING PLANT ASPARAGINE SYNTHETASE  
NUMBER OF SEQUENCES: 17  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/514, 816  
FILING DATE: 26-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 347,302  
FILING DATE: 03-MAY-1989  
SEQ ID NO: 7:  
LENGTH: 1121  
5256558-7

Query Match 3.1%; Score 17; DB 6; Length 1121;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 336 AGTATGTTTCTTAT.352  
|||||

Db 798 AGTATGTTTCTTAT 782

RESULT 6  
US-08-549-515-4  
Sequence 4, Application US/08549515  
Patent No. 6054123  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena M  
APPLICANT: Klein, Michael H  
TITLE OF INVENTION: Haemophilus Influenzae  
TITLE OF INVENTION: Dimethylsulphoxide Reductase Enzyme  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Slim & McBurney  
STREET: Suite 701, 330 Unversity Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/549, 515  
FILING DATE: 27-OCT-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-522  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 837 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-549-515-4

Query Match 2.9%; Score 16; DB 3; Length 837;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 112 TGGAAATATGCAATTA 127  
|||||

Db 430 TGGAAATATGCAATTA 445

RESULT 7  
US-08-897-340-4/c  
Sequence 4, Application US/08897340  
Patent No. 5955306  
GENERAL INFORMATION:  
APPLICANT: Gimeno, Carlos J. and Errada, Patrick, R.  
TITLE OF INVENTION: Weight Control Pathway Genes and Uses  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/897,340  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/715,032  
FILING DATE: 17-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Silverl, Jean M.  
REGISTRATION NUMBER: 39,030  
REFERENCE/DOCKET NUMBER: MNI-005CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1700 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-897-340-4

Query Match 2.9%; Score 16; DB 2; Length 1700;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 CAGTATGTTTCTT 350  
|||||

Db 1604 CAGTATGTTTCTT 1589

RESULT 8  
US-09-252-329-4/c  
Sequence 4, Application US/09252329  
Patent No. 6147192  
GENERAL INFORMATION:  
APPLICANT: Gimeno, Carlos J. and Errada, Patrick, R.  
TITLE OF INVENTION: Weight Control Pathway Genes and Uses  
Therefor

NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/252,329  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/897,340  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Silverl, Jean M.  
REGISTRATION NUMBER: 39,030  
REFERENCE/DOCKET NUMBER: MNT-005CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1700 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-252-329-4

Query Match 2.9%; Score 16; DB 4; Length 1700;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 CAGTATGTTTCTTCT 350  
DB 1604 CAGTATGTTTCTTCT 1589

RESULT 9  
US-08-464-340A-3/C  
Sequence 3, Application US/08464340A  
Patent No. 5710019  
GENERAL INFORMATION:  
APPLICANT: LI, ET AL.  
TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARIELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,340A  
FILING DATE: June 5, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/08449

FILING DATE: 28 JUL 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-415  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2483 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: cDNA  
US-08-464-340A-3

Query Match 2.9%; Score 16; DB 1; Length 2483;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 CTATCTGATGTCGTC 98  
DB 760 CTATCTGATGTCGTC 745

RESULT 10  
PCT-US94-08449A-3/C  
Sequence 3, Application PC/TUS9408449A  
GENERAL INFORMATION:  
APPLICANT: LI, ET AL.  
TITLE OF INVENTION: Potassium Channel Protein 1 and 2  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARIELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/08449A  
FILING DATE: SUBMITTED HERewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2483 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: cDNA  
PCT-US94-08449A-3

Query Match 2.9%; Score 16; DB 5; Length 2483;  
Best Local Similarity 100.0%; Pred. No. 32;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 CTATCTCTATGTCGTC 98  
|||||

Db 760 CTATCTCTATGTCGTC 745

RESULT 11  
US-08-703-809-2/c  
; Sequence 2, Application US/08703809  
; Patent No. 5716808  
; GENERAL INFORMATION:  
; APPLICANT: Raymond, Christopher K.  
; TITLE OF INVENTION: GENETIC ENGINEERING OF PICHIA METHANOLICA  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
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; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/703,809  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31-648  
; REFERENCE/DOCKET NUMBER: 96-18  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3386 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
US-08-703-809-2

Query Match 2.9%; Score 16; DB 1; Length 3386;  
Best Local Similarity 100.0%; Pred. NO. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 205 GTTATAGTTGCTTTAA 220  
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Db 1225 GTTATAGTTGCTTTAA 1210

RESULT 12  
US-08-703-808-2/c  
; Sequence 2, Application US/08703808  
; Patent No. 5736383  
; GENERAL INFORMATION:  
; APPLICANT: Raymond, Christopher K.  
; TITLE OF INVENTION: PREPARATION OF PICHIA METHANOLICA AUXOTROPHIC  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East

; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/703,808  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31-648  
; REFERENCE/DOCKET NUMBER: 96-17  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3386 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
US-08-703-808-2

Query Match 2.9%; Score 16; DB 1; Length 3386;  
Best Local Similarity 100.0%; Pred. NO. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 205 GTTATAGTTGCTTTAA 220  
|||||

Db 1225 GTTATAGTTGCTTTAA 1210

RESULT 13  
US-08-914-066-2/c  
; Sequence 2, Application US/08914066  
; Patent No. 5854039  
; GENERAL INFORMATION:  
; APPLICANT: Raymond, Christopher K.  
; APPLICANT: Holderman, Susan D.  
; APPLICANT: Vanaja, Erica  
; TITLE OF INVENTION: TRANSFORMATION OF PICHIA METHANOLICA  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/914,066  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E.  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-37

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3386 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-914-066-2

Query Match 2.9%; Score 16; DB 2; Length 3386;  
Best local Similarity 100.0%; Pred. No. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 GTTATAGTTGGTTAA 220  
|||||  
DB 1225 GTTATAGTTGGTTAA 1210

RESULT 14  
US-08-703-807-2/C  
Sequence 2, Application US/08703807  
Patent No. 5955349  
GENERAL INFORMATION:  
APPLICANT: Raymond, Christopher K.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCING  
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDES IN PICHIA METHANOLICA  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/703,807  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E  
REGISTRATION NUMBER: 31-648  
REFERENCE/DOCKET NUMBER: 96-16  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3386 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-703-807-2

Query Match 2.9%; Score 16; DB 2; Length 3386;

Best local Similarity 100.0%; Pred. No. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 205 GTTATAGTTGGTTAA 220  
|||||  
DB 1225 GTTATAGTTGGTTAA 1210

RESULT 15  
US-08-747-108A-2/C  
Sequence 2, Application US/08747108A  
Patent No. 5965389  
GENERAL INFORMATION:  
APPLICANT: Raymond, Christopher K.  
APPLICANT: Bukowski, Thomas R.  
APPLICANT: Bishop, Paul D.  
TITLE OF INVENTION: PRODUCTION OF GAD65 IN METHYLOTROPHIC YEAST  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 98111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,108A  
FILING DATE: 96-NOV-08  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-23-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-576-0200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3386 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-747-108A-2

Query Match 2.9%; Score 16; DB 2; Length 3386;  
Best local Similarity 100.0%; Pred. No. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 205 GTTATAGTTGGTTAA 220  
|||||  
DB 1225 GTTATAGTTGGTTAA 1210

Search completed: May 31, 2001, 02:15:13  
Job time: 4444 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2001, 23:54:33 ; Search time 1105.94 Seconds  
(without alignments)  
4384.085 Million cell updates/sec

Title: us-09-382-242-23

Perfect score: 555

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Gapop 60.0 , Gapext 60.0

Searched: 9623517 seqs, 4368049070 residues

Word size : 0

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	20	3.6	404	170	BF906208	BF906208 IL3-MT026
5	20	3.6	667	223	A2502214	A2502214 IM0341301
6	20	3.6	688	212	A0854708	A0854708 CPg2172A
7	20	3.6	771	230	CNS01VPE	AL169403 Tetraodon
8	20	3.6	983	230	CNS03B2I	AL237159 Tetraodon
9	20	3.6	1016	231	CNS0421Y	AL270943 Tetraodon
10	20	3.6	1019	231	CNS03009	AL253602 Tetraodon
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12	19	3.4	265	174	BG148611	BG148611 uu84g06.y
13	19	3.4	288	159	X61840	X61840 MOSTSG129X
14	19	3.4	291	129	BB266564	BB266564 BB266564
15	19	3.4	302	148	BF460484	BF460484 UI-M-CG0P
16	19	3.4	326	19	AI363223	AI363223 qv56b01.x
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18	19	3.4	388	208	AQ567554	AQ567554 HS_2118_B

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22	19	3.4	462	4	AA260892	AA260892	va01h12.r	95	18	3.2	355	227	B43580
23	19	3.4	486	103	A1875162	A1875162	u130c07.x	96	18	3.2	356	167	BE502815
24	19	3.4	497	145	BE228048	BE228048	uz39a12.x	97	18	3.2	356	213	AQ919017
25	19	3.4	502	203	AQ236170	AQ236170	HS_-2058_B	98	18	3.2	357	220	AZ387436
26	19	3.4	510	203	AQ180776	AQ180776	HS_-3220_A	99	18	3.2	358	18	A1290798
27	19	3.4	533	220	AZ365242	AZ365242	1M011N14	100	18	3.2	359	164	BE220020
28	19	3.4	534	206	AQ439999	AQ439999	HS_5073_A	101	18	3.2	361	102	A1806105
29	19	3.4	557	3	AA212780	AA212780	mB48e07.r	102	18	3.2	363	167	BE465398
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31	19	3.4	588	162	BE111788	BE111788	U1-R-BJ1-	104	18	3.2	364	226	AZ737138
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33	19	3.4	629	224	AZ624727	AZ624727	1M0463A15	106	18	3.2	379	215	AZ030575
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36	19	3.4	740	203	AQ194413	AQ194413	RPCI11-45	109	18	3.2	389	32	AM020928
37	19	3.4	794	226	B02432	B02432	CSR1-15e12	110	18	3.2	393	226	AZ748353
38	19	3.4	113	218	AZ224689	AZ224689	RPCI-23-6	111	18	3.2	399	103	A1913486
39	18	3.2	118	218	AZ259802	AZ259802	RPCI-23-1	112	18	3.2	401	215	AZ029663
40	18	3.2	132	114	AM325382	AM325382	16330_MAR	113	18	3.2	403	153	H71945
41	18	3.2	133	222	AZ482850	AZ482850	1M0308F07	114	18	3.2	403	226	AZ715894
42	18	3.2	137	216	AZ083432	AZ083432	RPCI-23-5	115	18	3.2	404	220	AZ372443
43	18	3.2	145	218	AZ240661	AZ240661	RPCI-23-7	116	18	3.2	405	223	AZ562251
44	18	3.2	147	216	AZ113521	AZ113521	RPCI-23-4	117	18	3.2	408	214	AQ986297
45	18	3.2	160	226	AZ720211	AZ720211	RPCI-24-1	118	18	3.2	411	223	AZ563016
46	18	3.2	167	216	AZ116215	AZ116215	RPCI-23-4	119	18	3.2	415	218	AZ266835
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54	18	3.2	223	226	AZ704685	AZ704685	RPCI-23-2	127	18	3.2	423	218	AZ245869
55	18	3.2	228	218	AZ282258	AZ282258	RPCI-23-1	128	18	3.2	424	226	AZ737924
56	18	3.2	230	221	AZ411190	AZ411190	1M0184H07	129	18	3.2	426	221	AZ401163
57	18	3.2	236	218	AZ259028	AZ259028	RPCI-23-1	130	18	3.2	430	223	AZ555575
58	18	3.2	239	226	AZ742810	AZ742810	RPCI-24-1	131	18	3.2	430	229	CNSO00US
59	18	3.2	251	226	AZ747559	AZ747559	RPCI-24-9	132	18	3.2	431	214	AQ987979
60	18	3.2	253	218	AZ276666	AZ276666	RPCI-23-1	133	18	3.2	431	214	AZ006374
61	18	3.2	256	214	AQ983564	AQ983564	RPCI-23-3	134	18	3.2	431	218	AZ251064
62	18	3.2	256	226	AZ719156	AZ719156	RPCI-24-7	135	18	3.2	432	216	AZ114730
63	18	3.2	261	28	AV329696	AV329696	AV329696	136	18	3.2	434	201	AQ055399
64	18	3.2	262	214	AZ013629	AZ013629	RPCI-23-2	137	18	3.2	435	214	AQ982226
65	18	3.2	265	215	AZ064469	AZ064469	RPCI-23-4	138	18	3.2	436	214	AZ009332
66	18	3.2	266	218	AZ282824	AZ282824	RPCI-23-1	139	18	3.2	436	216	AZ099089
67	18	3.2	272	218	AZ231992	AZ231992	RPCI-23-8	140	18	3.2	437	214	AQ976760
68	18	3.2	275	102	A1825156	A1825156	wa93b08.x	141	18	3.2	438	214	AZ011981
69	18	3.2	277	213	AQ928602	AQ928602	RPCI-23-2	142	18	3.2	438	218	AZ247682
70	18	3.2	279	229	CNSO00ES	AL083099	ArabiIdops	143	18	3.2	438	221	AZ395428
71	18	3.2	287	221	AZ420051	AZ420051	1M0196M14	144	18	3.2	438	224	AZ631727
72	18	3.2	289	214	AZ001421	AZ001421	RPCI-23-3	145	18	3.2	443	218	AZ233637
73	18	3.2	294	226	AZ718988	AZ718988	RPCI-24-1	146	18	3.2	444	205	AQ335676
74	18	3.2	295	215	AZ076745	AZ076745	RPCI-23-4	147	18	3.2	444	221	AZ444543
75	18	3.2	298	215	AZ027796	AZ027796	RPCI-23-3	148	18	3.2	449	225	AZ641899
76	18	3.2	300	226	AZ718475	AZ718475	RPCI-24-1	149	18	3.2	450	213	AQ928758
77	18	3.2	310	129	BB258093	BB258093	HS58093	150	18	3.2	450	215	AZ016668
78	18	3.2	312	218	AZ267463	AZ267463	RPCI-23-1	151	18	3.2	450	226	AZ753606
79	18	3.2	314	218	AZ273456	AZ273456	RPCI-23-8	152	18	3.2	451	219	AZ295119
80	18	3.2	315	216	AZ096156	AZ096156	RPCI-23-4	153	18	3.2	452	213	AQ916497
81	18	3.2	316	208	AQ548184	AQ548184	RPCI-11-4	154	18	3.2	452	213	AQ914484
82	18	3.2	320	226	AZ722583	AZ722583	RPCI-24-9	155	18	3.2	454	120	AM818937
83	18	3.2	322	135	BB536188	BB536188	HS536188	156	18	3.2	454	215	AZ074421
84	18	3.2	326	226	AZ721677	AZ721677	RPCI-24-7	157	18	3.2	454	220	AZ349718
85	18	3.2	327	224	AZ610200	AZ610200	1M0435C24	158	18	3.2	457	213	AQ931339
86	18	3.2	336	160	BB549290	BB549290	CIT-HSP-205	159	18	3.2	460	119	AM757259
87	18	3.2	336	227	B79753	B79753	CIT-HSP-205	160	18	3.2	461	215	AZ043665
88	18	3.2	344	216	AZ094460	AZ094460	RPCI-23-4	161	18	3.2	462	218	AZ246478
89	18	3.2	346	202	AQ087226	AQ087226	HS_2200_A	162	18	3.2	462	219	AZ295610
90	18	3.2	349	226	AZ717950	AZ717950	RPCI-24-1	163	18	3.2	462	227	B79952
91	18	3.2	354	102	A1823385	A1823385	WMS3d10.x	164	18	3.2	464	222	AZ485120

165	18	3.2	466	226	Az712633	Az712633	RPCI-24-1	C 238	18	3.2	551	216	Az095093	Az095093	RPCI-23-4
C 166	18	3.2	467	20	A1434898	A1434898	RPCI-23-3	C 239	18	3.2	552	214	Az0978397	Az0978397	RPCI-23-3
C 167	18	3.2	467	210	Az004487	Az004487	RPCI-23-3	C 240	18	3.2	552	223	Az510422	Az510422	RPCI-23-3
C 168	18	3.2	468	224	Az611193	Az611193	IM0436A05	C 241	18	3.2	553	138	BE672435	BE672435	7a60904 x
C 169	18	3.2	471	137	BE655506	BE655506	UI-M-BH0	C 242	18	3.2	553	219	Az292238	Az292238	RPCI-23-1
C 170	18	3.2	471	226	Az739240	Az739240	RPCI-24-1	C 243	18	3.2	554	219	Az291506	Az291506	RPCI-23-1
C 171	18	3.2	472	213	Az013820	Az013820	nbe0045K	C 244	18	3.2	554	222	Az461909	Az461909	IM0269A06
C 172	18	3.2	474	167	BE501062	BE501062	7a36d09 x	C 245	18	3.2	555	214	Az0979246	Az0979246	RPCI-23-2
C 173	18	3.2	475	216	Az093932	Az093932	RPCI-23-4	C 246	18	3.2	556	223	Az559347	Az559347	RPCI-23-2
C 174	18	3.2	475	220	Az388756	Az388756	IM0148L20	C 247	18	3.2	558	218	BE716302	BE716302	saal8c03
C 175	18	3.2	476	225	Az639424	Az639424	IM0409J22	C 248	18	3.2	561	168	BE716302	BE716302	saal8c03
C 176	18	3.2	477	216	Az085526	Az085526	RPCI-23-3	C 249	18	3.2	563	215	Az021734	Az021734	RPCI-23-3
C 177	18	3.2	478	210	Az095415	Az095415	HS_2148.A	C 250	18	3.2	565	215	Az080645	Az080645	RPCI-23-3
C 178	18	3.2	479	223	Az555234	Az555234	RPCI-23-1	C 251	18	3.2	565	221	Az410398	Az410398	IM0182008
C 179	18	3.2	479	226	Az742733	Az742733	RPCI-24-1	C 252	18	3.2	570	8	AA516727	AA516727	vh84a11.r
C 180	18	3.2	480	211	Az008330	Az008330	HS_5261.B	C 253	18	3.2	570	209	Az0670144	Az0670144	HS_5332.B
C 181	18	3.2	480	218	Az237827	Az237827	RPCI-23-7	C 254	18	3.2	571	218	Az285046	Az285046	RPCI-23-1
C 182	18	3.2	481	214	Az008924	Az008924	RPCI-23-3	C 255	18	3.2	572	214	Az200286	Az200286	RPCI-23-3
C 183	18	3.2	482	219	Az294530	Az294530	RPCI-23-1	C 256	18	3.2	572	224	Az624233	Az624233	IM0462G15
C 184	18	3.2	483	218	Az231912	Az231912	RPCI-23-9	C 257	18	3.2	572	226	Az738666	Az738666	RPCI-24-1
C 185	18	3.2	484	215	Az051461	Az051461	RPCI-23-3	C 258	18	3.2	574	215	Az039495	Az039495	RPCI-23-3
C 186	18	3.2	484	220	Az383877	Az383877	IM0141M07	C 259	18	3.2	574	226	Az728890	Az728890	RPCI-24-1
C 187	18	3.2	486	214	Az0970725	Az0970725	RPCI-23-3	C 260	18	3.2	579	218	Az257423	Az257423	RPCI-23-1
C 188	18	3.2	491	218	Az255121	Az255121	RPCI-23-1	C 261	18	3.2	580	222	Az469583	Az469583	RPCI-23-3
C 189	18	3.2	492	215	Az016946	Az016946	RPCI-23-2	C 262	18	3.2	582	122	AW970853	AW970853	EST382936
C 190	18	3.2	492	215	Az040934	Az040934	RPCI-23-2	C 263	18	3.2	582	221	Az0403840	Az0403840	IM0171N24
C 191	18	3.2	494	219	Az304740	Az304740	IM0004M19	C 264	18	3.2	583	106	Az044979	Az044979	IM0044979
C 192	18	3.2	495	214	Az0986626	Az0986626	RPCI-23-3	C 265	18	3.2	584	221	Az031354	Az031354	RPCI-23-3
C 193	18	3.2	495	216	Az089856	Az089856	RPCI-23-7	C 266	18	3.2	584	225	Az407478	Az407478	RPCI-23-3
C 194	18	3.2	495	220	Az350511	Az350511	IM0088P02	C 267	18	3.2	585	215	Az028612	Az028612	RPCI-23-3
C 195	18	3.2	496	219	Az217256	Az217256	IM0035L13	C 268	18	3.2	585	215	Az032801	Az032801	RPCI-23-3
C 196	18	3.2	497	104	A1968179	A1968179	wu14a09 x	C 269	18	3.2	585	226	Az747516	Az747516	RPCI-24-9
C 197	18	3.2	499	24	A1762324	A1762324	w997a03 x	C 270	18	3.2	586	222	Az475088	Az475088	RPCI-23-4
C 198	18	3.2	499	226	Az723956	Az723956	RPCI-24-6	C 271	18	3.2	587	215	Az056228	Az056228	RPCI-23-2
C 199	18	3.2	502	224	Az616510	Az616510	IM0446C30	C 272	18	3.2	588	226	Az697723	Az697723	RPCI-23-2
C 200	18	3.2	503	213	Az0928048	Az0928048	RPCI-23-2	C 273	18	3.2	588	226	Az721802	Az721802	RPCI-24-1
C 201	18	3.2	503	226	Az705395	Az705395	RPCI-23-2	C 274	18	3.2	593	220	Az448154	Az448154	IM0084J05
C 202	18	3.2	504	214	Az003188	Az003188	RPCI-23-3	C 275	18	3.2	593	220	Az385324	Az385324	IM0143EL3
C 203	18	3.2	505	216	Az117295	Az117295	RPCI-23-4	C 276	18	3.2	593	227	B67184	B67184	CPe00008A CP
C 204	18	3.2	505	224	Az599821	Az599821	IM0416D24	C 277	18	3.2	594	221	Az440419	Az440419	IM0231002
C 205	18	3.2	506	217	Az162559	Az162559	SP_0072.A	C 278	18	3.2	595	226	Az751126	Az751126	RPCI-24-8
C 206	18	3.2	507	224	Az595692	Az595692	IM0408A05	C 279	18	3.2	596	221	Az434012	Az434012	IM0320N12
C 207	18	3.2	508	102	A1816914	A1816914	w335b08 x	C 280	18	3.2	597	222	Az489136	Az489136	IM0319H16
C 208	18	3.2	509	214	Az0994236	Az0994236	RPCI-23-3	C 281	18	3.2	599	215	Az035299	Az035299	RPCI-23-2
C 209	18	3.2	509	216	Az110671	Az110671	RPCI-23-4	C 282	18	3.2	599	221	Az398494	Az398494	IM0163J22
C 210	18	3.2	514	216	Az118513	Az118513	RPCI-23-4	C 283	18	3.2	599	226	Az706200	Az706200	RPCI-23-2
C 211	18	3.2	515	215	Az068592	Az068592	RPCI-23-9	C 284	18	3.2	601	218	Az255628	Az255628	RPCI-23-1
C 212	18	3.2	516	218	Az262631	Az262631	RPCI-23-8	C 285	18	3.2	601	220	Az391959	Az391959	IM0154B22
C 213	18	3.2	517	218	Az236841	Az236841	RPCI-23-8	C 286	18	3.2	602	220	Az358517	Az358517	IM0095D19
C 214	18	3.2	518	8	AA517196	AA517196	vh86c03.r	C 287	18	3.2	602	224	Az607310	Az607310	IM0429M09
C 215	18	3.2	519	225	Az653249	Az653249	IM0526O13	C 288	18	3.2	602	226	Az715640	Az715640	RPCI-24-1
C 216	18	3.2	520	148	BF433198	BF433198	7g59c09 x	C 289	18	3.2	604	226	Az715640	Az715640	RPCI-24-1
C 217	18	3.2	520	218	Az233277	Az233277	RPCI-23-5	C 290	18	3.2	604	223	Az513174	Az513174	IM0359K07
C 218	18	3.2	522	215	Az024319	Az024319	RPCI-23-3	C 291	18	3.2	607	219	Az303756	Az303756	IM00003P22
C 219	18	3.2	522	216	Az086371	Az086371	RPCI-23-3	C 292	18	3.2	608	219	Az232341	Az232341	IM0044C20
C 220	18	3.2	524	167	BE463995	BE463995	hy19608 x	C 293	18	3.2	608	224	Az607461	Az607461	IM0429K19
C 221	18	3.2	525	213	Az0930643	Az0930643	RPCI-23-2	C 294	18	3.2	609	226	Az719905	Az719905	RPCI-24-1
C 222	18	3.2	525	221	Az397270	Az397270	IM0162K10	C 295	18	3.2	608	215	Az034858	Az034858	RPCI-23-2
C 223	18	3.2	529	224	Az610217	Az610217	IM0435F24	C 296	18	3.2	611	219	Az297904	Az297904	RPCI-23-9
C 224	18	3.2	531	157	T799442	T799442	vh85h11.s1	C 297	18	3.2	615	222	Az451955	Az451955	IM0251L05
C 225	18	3.2	531	214	Az005985	Az005985	RPCI-23-3	C 298	18	3.2	615	226	Az728470	Az728470	RPCI-24-8
C 226	18	3.2	532	216	Az099345	Az099345	RPCI-23-4	C 299	18	3.2	616	221	Az415838	Az415838	IM0190K11
C 227	18	3.2	534	220	Az361977	Az361977	IM0106G21	C 300	18	3.2	617	220	Az352430	Az352430	IM0091G02
C 228	18	3.2	536	143	BF061874	BF061874	7K68C02 x	C 301	18	3.2	618	221	Az439925	Az439925	IM0230G18
C 229	18	3.2	537	226	Az719267	Az719267	RPCI-24-1	C 302	18	3.2	621	226	Az749215	Az749215	RPCI-24-1
C 230	18	3.2	538	219	Az299649	Az299649	RPCI-23-1	C 303	18	3.2	622	225	Az649140	Az649140	IM0518B09
C 231	18	3.2	538	223	Az555866	Az555866	RPCI-23-2	C 304	18	3.2	622	225	Az653208	Az653208	IM0526G14
C 232	18	3.2	539	222	Az473920	Az473920	IM0280L02	C 305	18	3.2	623	222	Az468939	Az468939	IM0282N08
C 233	18	3.2	542	226	Az745207	Az745207	RPCI-24-1	C 306	18	3.2	624	210	Az0726308	Az0726308	HS_5406.B
C 234	18	3.2	543	136	BE550129	BE550129	7b49a11.x	C 307	18	3.2	626	220	Az370322	Az370322	IM0121J17
C 235	18	3.2	544	222	Az500560	Az500560	IM0339D01	C 308	18	3.2	626	226	Az731119	Az731119	RPCI-24-1
C 236	18	3.2	546	216	Az085223	Az085223	RPCI-23-2	C 309	18	3.2	629	219	Az322853	Az322853	IM0044C10
C 237	18	3.2	548	220	Az348522	Az348522	IM0085C11	C 310	18	3.2	631	216	Az098314	Az098314	RPCI-23-1

311	18	3.2	632	226	A2720675	RPCT-24-7	384	18	3.2	840	226	A2744523	A2744523	RPCT-24-7
312	18	3.2	634	214	A2008243	RPCT-23-3	385	18	3.2	841	226	A2750730	A2750730	RPCT-24-1
313	18	3.2	634	224	A2613568	IM0442B04	386	18	3.2	864	225	A2676600	A2676600	EMH573TF
314	18	3.2	634	224	A2617995	IM0449G06	387	18	3.2	868	231	CNS03Y0J1	AL265684	TETRADON
315	18	3.2	636	223	A2551865	RPCT-23-2	388	18	3.2	912	141	BE896960	BE896960	601439492
316	18	3.2	639	220	A2347808	IM0084E01	389	18	3.2	913	223	A2540656	A2540656	ENTDK17TR
317	18	3.2	639	218	A2270186	RPCT-23-7	390	18	3.2	940	223	A2543766	A2543766	ENTDM38TR
318	18	3.2	639	220	A2379685	IM0135C02	391	18	3.1	124	17	A1231495	A1231495	EST28183
319	18	3.2	643	226	A2742169	RPCT-24-6	392	17	3.1	130	10	AA675452	AA675452	UT-R-B52
320	18	3.2	643	223	A2558537	RPCT-23-2	393	17	3.1	137	147	BF397150	BF397150	UT-R-B52
321	18	3.2	645	204	A0290276	nbxb0036L	394	17	3.1	147	123	BB048809	BB048809	Mouse Li-re
322	18	3.2	646	225	A2640217	IM0502B11	395	17	3.1	160	227	B07595	B07595	Mouse Li-re
323	18	3.2	647	226	A2746850	RPCT-24-6	396	17	3.1	166	215	A2039467	A2039467	RPCT-23-3
324	18	3.2	648	221	A2414263	IM018BD09	397	17	3.1	171	161	BE023208	BE023208	sm79H05.Y
325	18	3.2	648	224	A2600769	IM0418C16	398	17	3.1	179	104	A1943846	A1943846	614030B06
326	18	3.2	649	150	BE576836	602132852	399	17	3.1	184	225	A2663960	A2663960	IM0543E24
327	18	3.2	649	224	A2618885	IM0450N18	400	17	3.1	185	173	BG095482	BG095482	mac28E11.
328	18	3.2	650	224	A2613771	IM0443J14	401	17	3.1	194	7	AA471627	AA471627	MBACFX4G0
329	18	3.2	651	219	A2292998	RPCT-23-1	402	17	3.1	196	127	BB185161	BB185161	BB185161
330	18	3.2	654	215	A2037109	RPCT-23-2	403	17	3.1	197	17	A1166537	A1166537	xylem.est
331	18	3.2	657	226	A2731781	RPCT-24-1	404	17	3.1	197	216	A2102963	A2102963	RPCT-23-3
332	18	3.2	658	221	A2439398	IM0230J01	405	17	3.1	216	167	BE505757	BE505757	dc36d11.x
333	18	3.2	659	225	A2648260	IM0517M12	406	17	3.1	219	155	R50519	R50519	yj60H05.S1
334	18	3.2	661	225	A2634702	IM0490G11	407	17	3.1	220	134	BB498233	BB498233	BB498233
335	18	3.2	662	224	A2615364	IM044J009	408	17	3.1	224	29	AV380102	AV380102	AV380102
336	18	3.2	664	226	A2717292	RPCT-24-6	409	17	3.1	225	131	BB369898	BB369898	BB369898
337	18	3.2	665	225	A2657648	IM0534B06	410	17	3.1	228	29	AV379894	AV379894	AV379894
338	18	3.2	666	222	A2454669	IM0256P11	411	17	3.1	229	108	AV02165	AV02165	AV02165
339	18	3.2	667	220	A2377226	IM0131O22	412	17	3.1	235	108	AV026981	AV026981	AV026981
340	18	3.2	668	216	A2121261	RPCT-23-1	413	17	3.1	237	29	AV365926	AV365926	AV365926
341	18	3.2	668	222	A2464049	IM0273E18	414	17	3.1	238	29	AV356053	AV356053	AV356053
342	18	3.2	669	219	A2286385	RPCT-23-1	415	17	3.1	240	29	AV356058	AV356058	AV356058
343	18	3.2	670	205	AQ0390613	CITBI-EI-	416	17	3.1	242	29	AV356058	AV356058	AV356058
344	18	3.2	670	216	A2109083	RPCT-23-8	417	17	3.1	245	105	AL386823	AL386823	AL386823
345	18	3.2	672	215	A2036403	RPCT-23-2	418	17	3.1	250	25	AV175629	AV175629	AV175629
346	18	3.2	672	221	A2445765	IM0241D21	419	17	3.1	251	22	A1578976	A1578976	UI-R-AA0-
347	18	3.2	674	226	A2752315	RPCT-24-1	420	17	3.1	252	15	A1072331	A1072331	UI-R-C2-n
348	18	3.2	677	121	AW937711	QV3-DT004	421	17	3.1	252	27	AV280404	AV280404	AV280404
349	18	3.2	677	224	A2629468	IM0482A01	422	17	3.1	255	136	BE526480	BE526480	M65D12STM
350	18	3.2	688	222	A2498678	IM0336O03	423	17	3.1	258	29	AA249863	AA249863	y0706.seq
351	18	3.2	690	224	A2600356	IM0418G03	424	17	3.1	258	4	AV355730	AV355730	AV355730
352	18	3.2	690	225	A2653284	IM0525E23	425	17	3.1	258	112	AW213839	AW213839	u043f06.x
353	18	3.2	693	220	A2380812	IM0136K23	426	17	3.1	258	134	BB466449	BB466449	BB466449
354	18	3.2	694	221	A2409638	IM0181P16	427	17	3.1	260	29	AV360256	AV360256	AV360256
355	18	3.2	696	219	A2315318	IM0032D03	428	17	3.1	263	202	AQ103434	AQ103434	HS-3058_B
356	18	3.2	700	224	A2615032	IM0444H08	429	17	3.1	265	27	AV285089	AV285089	AV285089
357	18	3.2	701	220	A2368570	IM0118P11	430	17	3.1	267	162	BE100937	BE100937	UI-R-BJ1-
358	18	3.2	705	224	A2632074	IM0486T06	431	17	3.1	268	107	AV013071	AV013071	AV013071
359	18	3.2	708	226	A2723979	RPCT-24-7	432	17	3.1	269	23	A1704013	A1704013	UI-R-AC1-
360	18	3.2	708	226	A2753645	RPCT-24-6	433	17	3.1	269	154	N72139	N72139	yz98F05.S1
361	18	3.2	711	219	A2290224	RPCT-23-1	434	17	3.1	270	13	AA885113	AA885113	am31h10.s
362	18	3.2	712	205	AQ0390561	CITBI-EI-	435	17	3.1	271	108	AV030189	AV030189	AV030189
363	18	3.2	712	220	A2347235	IM0083D16	436	17	3.1	273	133	BB432815	BB432815	BB432815
364	18	3.2	713	226	A2728706	RPCT-24-1	437	17	3.1	273	141	BE953755	BE953755	UT-M-CC1-
365	18	3.2	717	224	A2582622	IM0376F12	438	17	3.1	273	142	BF020329	BF020329	u064c11.x
366	18	3.2	725	219	A2321333	IM0041M02	439	17	3.1	276	128	BB254846	BB254846	BB254846
367	18	3.2	727	226	A2724967	RPCT-24-9	440	17	3.1	277	109	AV120819	AV120819	AV120819
368	18	3.2	741	224	A2624308	IM0462K22	441	17	3.1	277	109	AV133143	AV133143	AV133143
369	18	3.2	744	221	A2446569	IM0243K02	442	17	3.1	277	138	BE690100	BE690100	u064c11.y
370	18	3.2	751	226	A2733081	RPCT-24-1	443	17	3.1	278	127	BB178819	BB178819	BB178819
371	18	3.2	751	226	A2753018	RPCT-24-1	444	17	3.1	278	130	BB353239	BB353239	BB353239
372	18	3.2	753	211	AQ0747910	HS-5536_A	445	17	3.1	280	25	AV165296	AV165296	AV165296
373	18	3.2	753	220	A2347652	IM0083O15	446	17	3.1	280	109	AV086090	AV086090	AV086090
374	18	3.2	776	226	A2741975	RPCT-24-1	447	17	3.1	282	103	A1873862	A1873862	u042f12.x
375	18	3.2	778	204	AQ258383	nbxb0020D	448	17	3.1	283	129	BB264664	BB264664	BB264664
376	18	3.2	778	223	A2557462	RPCT-23-2	449	17	3.1	284	27	AV295597	AV295597	AV295597
377	18	3.2	778	226	A2740253	RPCT-24-7	450	17	3.1	284	132	BB383484	BB383484	BB383484
378	18	3.2	797	226	A2740333	RPCT-24-7	451	17	3.1	286	130	BB305806	BB305806	BB305806
379	18	3.2	799	226	A2743005	RPCT-24-7	452	17	3.1	286	130	BB322013	BB322013	BB322013
380	18	3.2	799	226	A2749032	RPCT-24-8	453	17	3.1	287	28	BB311436	BB311436	BB311436
381	18	3.2	812	226	A2749078	RPCT-24-8	454	17	3.1	288	129	BB266808	BB266808	BB266808
382	18	3.2	814	217	A2198805	SR-1038_B	455	17	3.1	290	109	AV144669	AV144669	AV144669
383	18	3.2	838	216	A2090543	RPCT-23-2	456	17	3.1	290	109	AV144669	AV144669	AV144669

457	17	3.1	291	125	BB125483	BB125453	530	17	3.1	386	3	AA198202	AA198202	mv46e06.r
458	17	3.1	291	131	BB346170	BB346170	531	17	3.1	388	21	A1538659	A1538659	tp70h03.x
459	17	3.1	291	152	D64927	BB429494	532	17	3.1	389	22	A4452150	A4452150	IM0251B23
460	17	3.1	292	133	BB429494	BB429494	533	17	3.1	393	150	BE553014	BE553014	UI-R-C2-n
461	17	3.1	293	126	BB173860	BB173860	534	17	3.1	393	164	BE197964	BE197964	uq77c08.x
462	17	3.1	293	130	BB322163	BB322163	535	17	3.1	394	174	BB229882	BB229882	mac23h10.x
463	17	3.1	294	160	BB517195	BB517195	536	17	3.1	397	136	BE552669	BE552669	uq68g03.x
464	17	3.1	293	123	BB021863	BB021863	537	17	3.1	399	112	AW212880	AW212880	uq68g03.x
465	17	3.1	295	102	A1784670	la03e670.x	538	17	3.1	399	148	BF425162	BF425162	uq68g03.x
466	17	3.1	295	123	BB030730	BB030730	539	17	3.1	401	21	A1488093	A1488093	EST26401.Y
467	17	3.1	295	125	BB125214	BB125214	540	17	3.1	401	117	AM594361	AM594361	h966c04.x
468	17	3.1	295	128	BB245169	BB245169	541	17	3.1	401	203	AQ191234	AQ191234	HS_-2197_A
469	17	3.1	295	167	BE505521	dc31g01.x	542	17	3.1	403	167	BE475123	BE475123	sp72e07.Y
470	17	3.1	296	132	BB383342	BB383342	543	17	3.1	405	21	A1504357	A1504357	v108B04.x
471	17	3.1	296	132	BB389212	BB389212	544	17	3.1	405	174	BB168543	BB168543	602345219
472	17	3.1	297	125	AA290765	z423c05.s	545	17	3.1	408	11	AA737033	AA737033	nx90e05.s
473	17	3.1	297	125	BB103452	BB103452	546	17	3.1	408	207	AQ474664	AQ474664	CITB1-E1-
474	17	3.1	298	112	AAW12359	u085h02.x	547	17	3.1	409	10	AA638747	AA638747	ym85B09..r
475	17	3.1	299	156	T23528	secq3366.1-N	548	17	3.1	409	105	AL384417	AL384417	MCBC21H09
476	17	3.1	300	21	A1482165	vF51c03.x	549	17	3.1	409	138	BE690520	BE690520	u544h08.x
477	17	3.1	301	130	BB303629	BB303629	550	17	3.1	409	150	BF593107	BF593107	7049e07.x
478	17	3.1	301	130	BB365868	BB365868	551	17	3.1	409	233	BF508669	BF508669	1M03511.1
479	17	3.1	302	130	BB322390	BB322390	552	17	3.1	412	23	A1687112	A1687112	CP84f11.x
480	17	3.1	303	232	PC304241	PlasmModu	553	17	3.1	413	116	AM512889	AM512889	x004e07.x
481	17	3.1	304	127	BB188714	BB188714	554	17	3.1	413	163	BE133613	BE133613	uq03c03.x
482	17	3.1	305	107	AV007565	AV007565	555	17	3.1	414	214	AZ009260	AZ009260	RPCT-23-3
483	17	3.1	305	122	BB009230	BB009230	556	17	3.1	416	22	A1623742	A1623742	ts38g01.x
484	17	3.1	307	131	BB359277	BB359277	557	17	3.1	416	213	NO881110	NO881110	HS_5136.B
485	17	3.1	308	129	BB263614	BB263614	558	17	3.1	417	13	AA866251	AA866251	UI-R-A0-D
486	17	3.1	310	110	AA083596	xc19g08.x	559	17	3.1	417	111	AM124081	AM124081	UI-M-BH2
487	17	3.1	310	126	BB166297	BB166297	560	17	3.1	417	226	AZ75914	AZ75914	T221094.x
488	17	3.1	312	126	BB097898	BB097898	561	17	3.1	418	110	AM071483	AM071483	x444f01.x
489	17	3.1	312	126	BB144080	BB144080	562	17	3.1	418	122	AM987620	AM987620	uf26g12.x
490	17	3.1	312	129	BB285704	BB285704	563	17	3.1	419	23	A1684630	A1684630	wa84a08.x
491	17	3.1	313	125	BB095159	BB095159	564	17	3.1	421	3	AA169831	AA169831	z092a05.s
492	17	3.1	313	133	BB453819	BB453819	565	17	3.1	421	137	BE649173	BE649173	UI-M-BH2
493	17	3.1	314	21	A1553107	A1553107	566	17	3.1	422	7	AA456874	AA456874	aa38b11.r
494	17	3.1	314	126	BB172644	BB172644	567	17	3.1	422	30	AV428081	AV428081	AV019449
495	17	3.1	314	139	BE755209	208969.MA	568	17	3.1	422	106	AU019449	AU019449	AV019449
496	17	3.1	316	108	AAV02658	AAV02658	569	17	3.1	422	162	BE057776	BE057776	uq7a08.Y
497	17	3.1	316	126	BB146810	BB146810	570	17	3.1	422	202	AA090669	AA090669	HS_3010.A
498	17	3.1	320	134	BB464028	BB464028	571	17	3.1	429	114	AM382883	AM382883	PM1-H103.A
499	17	3.1	320	172	BB043527	BB043527	572	17	3.1	429	215	AZ038338	AZ038338	RPCT-23-3
500	17	3.1	321	109	AAV114960	AAV114960	573	17	3.1	437	16	A1102128	A1102128	EST211417
501	17	3.1	322	107	AAV007398	AAV007398	574	17	3.1	437	206	AQ443164	AQ443164	HS_5130.A
502	17	3.1	324	132	BB391630	BB391630	575	17	3.1	438	225	AZ652145	AZ652145	1M0525C18
503	17	3.1	326	125	BB120888	BB120888	576	17	3.1	443	150	BF565095	BF565095	UI-R-B01-
504	17	3.1	326	133	BB446851	BB446851	577	17	3.1	445	105	AL370611	AL370611	MCBA38H03
505	17	3.1	329	9	AA535055	AA535055	578	17	3.1	447	102	A1849437	A1849437	UI-M-AJ1-
506	17	3.1	329	124	BB085051	BB085051	579	17	3.1	448	3	AA200134	AA200134	ml10b11.r
507	17	3.1	331	165	BE288929	h932c12.x	580	17	3.1	448	117	AM601321	AM601321	PMO-BT034
508	17	3.1	336	133	BB447032	BB447032	581	17	3.1	450	13	AA875396	AA875396	UI-R-E0-C
509	17	3.1	337	20	A1443891	A1443891	582	17	3.1	450	140	BE851966	BE851966	u412a02.x
510	17	3.1	338	160	BB546751	BB546751	583	17	3.1	450	203	AQ243283	AQ243283	HS_-2064_A
511	17	3.1	339	12	AA134487	AA134487	584	17	3.1	451	203	AQ185231	AQ185231	HS_-2229-B
512	17	3.1	349	12	AA818312	AA818312	585	17	3.1	453	202	AQ112140	AQ112140	CIT-HSB-2
513	17	3.1	360	3	AA169651	AA169651	586	17	3.1	454	19	A1392627	A1392627	CG40e02.x
514	17	3.1	360	22	AA160289	AA160289	587	17	3.1	455	164	BE200375	BE200375	uq61e07.x
515	17	3.1	360	25	AA196159	AA196159	588	17	3.1	456	105	AL367999	AL367999	MCBA21E09
516	17	3.1	360	31	AAV655460	AAV655460	589	17	3.1	456	222	AZ478710	AZ478710	IM0298P23
517	17	3.1	360	175	CC65523	CC65523	590	17	3.1	457	114	AAW358714	AAW358714	43450.MAR
518	17	3.1	362	7	AA420078	AA420078	591	17	3.1	457	120	AAW821740	AAW821740	RC4-ST031
519	17	3.1	365	12	AA836363	AA836363	592	17	3.1	457	226	AZ737006	AZ737006	RPCT-24-1
520	17	3.1	366	202	AA0088326	AA0088326	593	17	3.1	459	207	AA0484285	AA0484285	RPCT-11-2
521	17	3.1	368	5	AA215032	AA215032	594	17	3.1	460	122	AAW990495	AAW990495	u0f0601.x
522	17	3.1	369	5	AA307491	AA307491	595	17	3.1	462	140	BE861811	BE861811	UI-M-AH1-x
523	17	3.1	369	22	AA1615491	AA1615491	596	17	3.1	462	173	BB133820	BB133820	EST466712
524	17	3.1	371	10	AA645908	AA645908	597	17	3.1	462	211	AA0765069	AA0765069	HS_3153.B
525	17	3.1	372	214	AA0971013	AA0971013	598	17	3.1	463	137	BE626194	BE626194	u0f8408.x
526	17	3.1	374	9	AA6525777	AA6525777	599	17	3.1	466	213	AA0919663	AA0919663	RPCT-23-2
527	17	3.1	375	16	AA1152348	AA1152348	600	17	3.1	471	17	A1235334	A1235334	EST231896
528	17	3.1	381	20	AA1407208	AA1407208	601	17	3.1	472	223	AZ504548	AZ504548	IM0344123
529	17	3.1	382	148	BF425158	BF425158	602	17	3.1	473	163	BE186204	BE186204	945037E08

C 603	17	3.1	474	18	AI280708	AI280708 qw10d08.x	C 676	17	3.1	564	30	AV537441	AV537441 AV537441
C 604	17	3.1	475	163	BE121659	BE121659 894014A05	C 677	17	3.1	564	223	A2558672	A2558672 RPT-23-2
C 605	17	3.1	475	205	AQ353020	AQ353020 CITBI-E1-	C 678	17	3.1	567	167	BE440609	BE440609 sp47g12.y
C 606	17	3.1	476	3	AA184998	AA184998 mt18BD10..r	C 679	17	3.1	569	117	AM551230	AM551230 L0075E12
C 607	17	3.1	476	115	AA452347	AA452347 UT-H-B13-	C 680	17	3.1	571	121	AM860475	AM860475 QV0-CT038
C 608	17	3.1	478	19	AI379663	AI379663 tc60a02.x	C 681	17	3.1	572	167	BE457691	BE457691 us95e11.x
C 609	17	3.1	478	111	AM158544	AM158544 xt76b05.x	C 682	17	3.1	573	172	BE070658	BE070658 H308G02-
C 610	17	3.1	478	219	A2298231	A2298231 RPT-23-1	C 683	17	3.1	577	13	AA875001	AA875001 UT-R-E0-C
C 611	17	3.1	479	150	BE615836	BE615836 dd97a02.y	C 684	17	3.1	577	15	AI072007	AI072007 UT-R-C2-n
C 612	17	3.1	479	163	BE119525	BE119525 UT-R-CM0-	C 685	17	3.1	582	141	BE938958	BE938958 PM4-TN011
C 613	17	3.1	480	173	BE133083	BE133083 EST465975	C 686	17	3.1	582	141	BE938975	BE938975 PM4-TN011
C 614	17	3.1	481	207	AO507835	AO507835 RPT-11-2	C 687	17	3.1	582	150	BE55111	BE55111 UT-R-E0-C
C 615	17	3.1	481	226	A2753114	A2753114 RPT-24-1	C 688	17	3.1	584	163	BE188687	BE188687 db58d04.x
C 616	17	3.1	482	111	AM144023	AM144023 EST294319	C 689	17	3.1	584	221	A2444083	A2444083 LM0239E08
C 617	17	3.1	482	148	BE416423	BE416423 UT-R-CM0-	C 690	17	3.1	585	118	AM646146	AM646146 cm61d04..w
C 618	17	3.1	484	119	AM761593	AM761593 sl69g02.y	C 691	17	3.1	589	121	AM875242	AM875242 RCI-PT000
C 619	17	3.1	484	162	BE097267	BE097267 UT-R-B01-	C 692	17	3.1	590	30	AV602491	AV602491 AV602491
C 620	17	3.1	484	169	BE845930	BE845930 QV1-EN005	C 693	17	3.1	592	224	A2611540	A2611540 LM0437R22
C 621	17	3.1	485	162	BE109533	BE109533 UT-R-B01-	C 694	17	3.1	594	15	AI012640	AI012640 EST207091
C 622	17	3.1	486	2	AA114682	AA114682 nm04H09..r	C 695	17	3.1	595	18	AI264355	AI264355 q109e12.x
C 623	17	3.1	487	214	AO980312	AO980312 RPT-23-3	C 696	17	3.1	595	218	A2260854	A2260854 RPT-23-1
C 624	17	3.1	492	113	AM266712	AM266712 L48-4373	C 697	17	3.1	596	219	A2320925	A2320925 LM0041N11
C 625	17	3.1	492	150	BE554928	BE554928 UT-R-E0-C	C 698	17	3.1	596	225	A2650049	A2650049 LM0520F03
C 626	17	3.1	494	16	AI102227	AI102227 EST211516	C 699	17	3.1	597	103	AI883192	AI883192 fd17g10.y
C 627	17	3.1	496	32	AV735007	AV735007 AV735007	C 700	17	3.1	597	136	BE510452	BE510452 946053A06
C 628	17	3.1	497	17	AI233151	AI233151 EST229839	C 701	17	3.1	599	106	AU016695	AU016695 AU016695
C 629	17	3.1	497	138	BE691742	BE691742 uv66a08.x	C 702	17	3.1	601	105	AI138227	AI138227 DKF2P547A
C 630	17	3.1	500	107	AU086363	AU086363 AU086363	C 703	17	3.1	602	105	AI138236	AI138236 DKF2P547C
C 631	17	3.1	500	220	A2385156	A2385156 LM0143R02	C 704	17	3.1	603	21	AI148236	AI148236 DKF2P547C
C 632	17	3.1	502	16	AI103693	AI103693 EST212982	C 705	17	3.1	603	24	AI1742057	AI1742057 w938d12.x
C 633	17	3.1	503	216	A2144431	A2144431 SP_-0009_A	C 706	17	3.1	605	118	AM676613	AM676613 833009C03
C 634	17	3.1	503	226	A2737830	A2737830 RPT-24-1	C 707	17	3.1	605	225	A2646024	A2646024 LM0511A20
C 635	17	3.1	504	112	AM209219	AM209219 uc07e03.x	C 708	17	3.1	607	116	AM531913	AM531913 UT-R-B50-
C 636	17	3.1	504	205	AQ359254	AQ359254 HS_5030_B	C 709	17	3.1	607	174	BE616803	BE616803 de43d03.x
C 637	17	3.1	505	206	AO434021	AO434021 HS_5084_A	C 710	17	3.1	610	137	AM761135	AM761135 sl63f11.y
C 638	17	3.1	506	103	AI884446	AI884446 vm32f01.x	C 711	17	3.1	610	137	BE598519	BE598519 P11_83_E0
C 639	17	3.1	508	24	AI733081	AI733081 oJ26H04..x	C 712	17	3.1	611	16	AI125430	AI125430 qd93d10..x
C 640	17	3.1	509	16	AI132702	AI132702 uc33g03.x	C 713	17	3.1	611	163	BE121660	BE121660 894014A05
C 641	17	3.1	509	122	AM989356	AM989356 uf25b09.y	C 714	17	3.1	613	9	AA611588	AA611588 v093B08..r
C 642	17	3.1	509	221	A2444432	A2444432 LM0239E08	C 715	17	3.1	621	165	BE337321	BE337321 894045H12
C 643	17	3.1	510	211	AQ73878	AQ73878 HS_2050_A	C 716	17	3.1	621	202	AO109803	AO109803 CIT-HSP-2
C 644	17	3.1	511	149	BE549145	BE549145 UT-R-A0-A	C 717	17	3.1	623	164	BE239882	BE239882 EST403931
C 645	17	3.1	511	214	AO995569	AO995569 RPT-23-3	C 718	17	3.1	624	13	AA892376	AA892376 EST196179
C 646	17	3.1	513	22	AI599160	AI599160 EST250863	C 719	17	3.1	629	121	AM875250	AM875250 RCI-PT000
C 647	17	3.1	515	110	AM070200	AM070200 xa09b06.x	C 720	17	3.1	630	215	A2071278	A2071278 RPT-23-3
C 648	17	3.1	516	143	BE044341	BE044341 xA09b06..x	C 721	17	3.1	632	148	BF424769	BF424769 su50c06.y
C 649	17	3.1	519	20	AI1410239	AI1410239 EST38532	C 722	17	3.1	634	218	A2268016	A2268016 RPT-23-1
C 650	17	3.1	520	12	AA800588	AA800588 EST190085	C 723	17	3.1	637	78	BE237813	BE237813 RPT-23-1
C 651	17	3.1	520	13	AA886892	AA886892 oJ26H04..s	C 724	17	3.1	642	78	BE317549	BE317549 NF051D04L
C 652	17	3.1	525	116	AM533564	AM533564 UT-R-B50-	C 725	17	3.1	643	205	AQ345998	AQ345998 RPT-23-4
C 653	17	3.1	526	204	AQ262879	AQ262879 CITBI-E1-	C 726	17	3.1	652	202	AQ082082	AQ082082 RPT-11-12
C 654	17	3.1	526	205	AQ358402	AQ358402 HS_5028_A	C 727	17	3.1	656	173	BE073644	BE073644 H3126D08-
C 655	17	3.1	530	112	AM215393	AM215393 up03b07.x	C 728	17	3.1	658	218	A2273121	A2273121 RPT-23-1
C 656	17	3.1	534	206	AO427195	AO427195 CITBI-E1-	C 729	17	3.1	658	220	A2363813	A2363813 LM0109106
C 657	17	3.1	535	208	AO570028	AO570028 HS_5370_A	C 730	17	3.1	661	112	AM185365	AM185365 sp38d07.y
C 658	17	3.1	538	119	AM721773	AM721773 833010A12	C 731	17	3.1	661	165	BE347445	BE347445 sp38d07.y
C 659	17	3.1	539	119	AM707849	AM707849 832013C08	C 732	17	3.1	664	225	A2660202	A2660202 LM0538110
C 660	17	3.1	540	164	BE237812	BE237812 894038D04	C 733	17	3.1	668	206	AQ423538	AQ423538 CITBI-E1-
C 661	17	3.1	541	218	AZ256765	AZ256765 RPT-23-1	C 734	17	3.1	674	218	A2261019	A2261019 RPT-23-1
C 662	17	3.1	543	141	BE930790	BE930790 RCI-GN007	C 735	17	3.1	683	240	A2375387	A2375387 LM0128010
C 663	17	3.1	545	228	B92965	B92965 CIT-HSP-216	C 736	17	3.1	690	24	AI177377	AI177377 EST263785
C 664	17	3.1	546	136	BE510451	BE510451 946053A06	C 737	17	3.1	690	204	AQ274694	AQ274694 RPT-4-61
C 665	17	3.1	546	162	BE104165	BE104165 UT-R-BX0-	C 738	17	3.1	694	174	BE165741	BE165741 602344586
C 666	17	3.1	547	205	AQ351195	AQ351195 RPT-11-12	C 739	17	3.1	695	219	A2296644	A2296644 RPT-23-3
C 667	17	3.1	547	111	AM144344	AM144344 EST294640	C 740	17	3.1	699	217	A2398644	A2398644 RPT-23-3
C 668	17	3.1	547	210	AO683125	AO683125 HS_5378_B	C 741	17	3.1	700	215	A2038494	A2038494 RPT-23-3
C 669	17	3.1	548	224	A2630724	A2630724 LM0484M23	C 742	17	3.1	704	220	AZ349685	AZ349685 LM0086114
C 670	17	3.1	549	117	AM556131	AM556131 L0264C07-	C 743	17	3.1	713	173	BE128146	BE128146 EST473792
C 671	17	3.1	551	216	A2146702	A2146702 SP_5043_B	C 744	17	3.1	721	174	BE620791	BE620791 602362025
C 672	17	3.1	553	211	AQ799420	AQ799420 HS_5400_B	C 745	17	3.1	726	137	BE620791	BE620791 601483535
C 673	17	3.1	554	210	AQ726032	AQ726032 HS_5400_B	C 746	17	3.1	738	23	AI692200	AI692200 wd37h09.x
C 674	17	3.1	555	20	AI435473	AI435473 ch94H01..x	C 747	17	3.1	739	114	AM348708	AM348708 GM210003A
C 675	17	3.1	561	217	A2149211	A2149211 SP_0046_A	C 748	17	3.1	739	114	AM348708	AM348708 GM210003A

C 749	17	3.1	741	230	CNS0242B	AL180236	Tetraodon	C 822	16	2.9	209	127	BB213255	BB213255
C 750	17	3.1	761	220	AZ347194	AZ347194	IN0083M07	C 823	16	2.9	213	16	A1130158	A1130158
C 751	17	3.1	764	139	BE789512	BE789512	601481204	C 824	16	2.9	217	160	BB569832	BB569832
C 752	17	3.1	770	210	AO740787	AO740787	HS-5508.A	C 825	16	2.9	218	124	BB068410	BB068410
C 753	17	3.1	776	107	AU117134	AU117134	ANT117134	C 826	16	2.9	221	130	BB288573	BB288573
C 754	17	3.1	778	14	AI001351	AI001351	MEST7-C5.	C 827	16	2.9	224	159	Z21883	Z21883
C 755	17	3.1	782	218	AZ238727	AZ238727	RPCI-23-B	C 828	16	2.9	225	26	AV223886	AV223886
C 756	17	3.1	782	226	B01640	B01640	CSRL-135b-6	C 829	16	2.9	227	8	AA522550	AA522550
C 757	17	3.1	785	226	AZ744220	AZ744220	RPCI-24-1	C 830	16	2.9	227	126	BB148106	BB148106
C 758	17	3.1	789	217	AZ184836	AZ184836	SP-1003.B	C 831	16	2.9	229	132	BB412906	BB412906
C 759	17	3.1	799	166	BE383171	BE383171	601298720	C 832	16	2.9	231	115	AM480208	AM480208
C 760	17	3.1	803	174	BG166207	BG166207	602340963	C 833	16	2.9	231	115	AM480208	AM480208
C 761	17	3.1	804	23	AV401119	AV401119	AV401119	C 834	16	2.9	237	108	AV058994	AV058994
C 762	17	3.1	819	225	AZ678447	AZ678447	ENTHPA1TF	C 835	16	2.9	238	110	AM078750	AM078750
C 763	17	3.1	830	223	AZ531176	AZ531176	ENTCS57TF	C 836	16	2.9	238	115	AM452315	AM452315
C 764	17	3.1	833	202	AO157178	AO157178	nbxb0009E	C 837	16	2.9	239	128	BB25752	BB25752
C 765	17	3.1	843	210	AO744441	AO744441	HS-5506.A	C 838	16	2.9	240	29	AV377359	AV377359
C 766	17	3.1	861	225	AZ684836	AZ684836	ENTGJ11TF	C 839	16	2.9	240	106	AU073997	AU073997
C 767	17	3.1	862	225	AZ681214	AZ681214	ENTH057TF	C 840	16	2.9	240	106	AU074304	AU074304
C 768	17	3.1	866	223	AZ551149	AZ551149	ENTH057TF	C 841	16	2.9	240	112	AM235769	AM235769
C 769	17	3.1	867	226	AZ692033	AZ692033	ENTKLE5TF	C 842	16	2.9	240	124	BB068769	BB068769
C 770	17	3.1	874	139	BE748510	BE748510	601571424	C 843	16	2.9	242	20	AI463647	AI463647
C 771	17	3.1	875	225	AZ677298	AZ677298	ENTIG59TF	C 844	16	2.9	242	122	BB012384	BB012384
C 772	17	3.1	880	223	AZ535801	AZ535801	ENTCA27TF	C 845	16	2.9	243	8	AA480371	AA480371
C 773	17	3.1	898	223	AZ528805	AZ528805	ENTCG83TF	C 846	16	2.9	244	110	AM039061	AM039061
C 774	17	3.1	898	223	AZ549697	AZ549697	ENTGA47TF	C 847	16	2.9	245	207	AO505700	AO505700
C 775	17	3.1	900	173	BG105527	BG105527	602312137	C 848	16	2.9	247	29	AV372997	AV372997
C 776	17	3.1	902	223	AZ540900	AZ540900	ENTFP65TF	C 849	16	2.9	247	172	BG056876	BG056876
C 777	17	3.1	904	22	AI607605	AI607605	VK47901.Y	C 850	16	2.9	249	32	AM007538	AM007538
C 778	17	3.1	909	223	AZ534129	AZ534129	ENTCF83TF	C 851	16	2.9	249	104	AI985665	AI985665
C 779	17	3.1	911	225	AZ679507	AZ679507	ENTUM43TF	C 852	16	2.9	249	201	AI066183	AI066183
C 780	17	3.1	933	225	AZ684926	AZ684926	ENTIE28TF	C 853	16	2.9	254	109	AV136150	AV136150
C 781	17	3.1	949	230	CNS039EV	CNS039EV	Teiraodon	C 854	16	2.9	254	107	AM633854	AM633854
C 782	17	3.1	959	173	BG115093	BG115093	602315928	C 855	16	2.9	255	120	AV006109	AV006109
C 783	17	3.1	965	106	AL524646	AL524646	AL524646	C 856	16	2.9	255	157	T94651	T94651
C 784	17	3.1	976	174	BG529094	BG529094	602379149	C 857	16	2.9	257	102	AI804813	AI804813
C 785	17	3.1	980	145	BE184785	BE184785	601844527	C 858	16	2.9	259	20	AI466293	AI466293
C 786	17	3.1	983	225	AZ683479	AZ683479	ENTM107TF	C 859	16	2.9	259	26	AV238735	AV238735
C 787	17	3.1	986	143	BF065197	BF065197	HY-CEB002	C 860	16	2.9	259	30	AV535718	AV535718
C 788	17	3.1	1029	221	CNS03XNI	CNS03XNI	Teiraodon	C 861	16	2.9	261	124	BB076725	BB076725
C 789	17	3.1	1038	217	AZ202973	AZ202973	SP-0079.B	C 862	16	2.9	264	29	AV366796	AV366796
C 790	17	3.1	1077	139	BE748748	BE748748	601571914	C 863	16	2.9	264	161	BB596660	BB596660
C 791	17	3.1	1088	232	CNS0500W	CNS0500W	Teiraodon	C 864	16	2.9	266	114	AM362507	AM362507
C 792	17	3.1	1201	145	BE183344	BE183344	601809435	C 865	16	2.9	267	11	AA762799	AA762799
C 793	16	2.9	105	22	AI604837	AI604837	me28908.x	C 866	16	2.9	267	172	BG049059	BG049059
C 794	16	2.9	114	229	CNS00Y3D	CNS00Y3D	Arabiadops	C 867	16	2.9	268	104	AI968297	AI968297
C 795	16	2.9	120	201	AF056258	AF056258	AF056258	C 868	16	2.9	269	215	AZ024714	AZ024714
C 796	16	2.9	120	110	AM091828	AM091828	EST285008	C 869	16	2.9	273	9	AA568480	AA568480
C 797	16	2.9	135	162	BE049435	BE049435	xw86e05.x	C 870	16	2.9	273	103	AI874013	AI874013
C 798	16	2.9	142	115	AM421180	AM421180	l193601.x	C 871	16	2.9	273	108	AV061303	AV061303
C 799	16	2.9	146	104	AI988489	AI988489	s602h12.y	C 872	16	2.9	276	26	AV246477	AV246477
C 800	16	2.9	147	218	AZ265686	AZ265686	RPCI-23-4	C 873	16	2.9	276	170	BF920115	BF920115
C 801	16	2.9	149	110	AM038547	AM038547	EST280230	C 874	16	2.9	276	172	BG019119	BG019119
C 802	16	2.9	150	27	AV267666	AV267666	AV267666	C 875	16	2.9	277	26	AV243147	AV243147
C 803	16	2.9	153	162	BE047432	BE047432	hg75e03.x	C 876	16	2.9	277	217	AZ187283	AZ187283
C 804	16	2.9	160	155	N93685	N93685	zb50h06.sl	C 877	16	2.9	279	2	AA144678	AA144678
C 805	16	2.9	162	10	AA646955	AA646955	vn38d10.r	C 878	16	2.9	279	126	BB143017	BB143017
C 806	16	2.9	162	150	BF597675	BF597675	su87d12.y	C 879	16	2.9	279	5	AA318797	AA318797
C 807	16	2.9	170	6	AA379986	AA379986	EST92888	C 880	16	2.9	279	158	W81564	W81564
C 808	16	2.9	174	109	AV083733	AV083733	AV083733	C 881	16	2.9	283	112	AM239138	AM239138
C 809	16	2.9	175	19	AI348396	AI348396	gq34b07.x	C 882	16	2.9	283	150	BF606438	BF606438
C 810	16	2.9	183	1	AA044925	AA044925	zk77b11.r	C 883	16	2.9	284	26	AV220929	AV220929
C 811	16	2.9	183	161	BB600438	BB600438	BB600438	C 884	16	2.9	284	109	AV112114	AV112114
C 812	16	2.9	190	152	D45600	D45600	HUMGS02792	C 885	16	2.9	284	119	AM765343	AM765343
C 813	16	2.9	191	109	AV122706	AV122706	AV122706	C 886	16	2.9	286	22	AI613015	AI613015
C 814	16	2.9	191	130	BB326334	BB326334	BB326334	C 887	16	2.9	286	27	AV296598	AV296598
C 815	16	2.9	192	218	AZ226708	AZ226708	RPCI-23-6	C 888	16	2.9	286	117	AM612259	AM612259
C 816	16	2.9	192	222	AZ483822	AZ483822	IM0309N15	C 889	16	2.9	286	118	AM659697	AM659697
C 817	16	2.9	199	127	BB207978	BB207978	BB207978	C 890	16	2.9	286	131	BB338202	BB338202
C 818	16	2.9	202	103	AI902226	AI902226	QV-ET003-8	C 891	16	2.9	286	154	N76786	N76786
C 819	16	2.9	205	129	BB275948	BB275948	BB275948	C 892	16	2.9	287	129	BB266136	BB266136
C 820	16	2.9	206	130	BB334105	BB334105	BB334105	C 893	16	2.9	287	130	BB307653	BB307653
C 821	16	2.9	208	108	AV016051	AV016051	AV016051	C 894	16	2.9	289	131	BB371271	BB371271



895	16	2.9	289	173	EG123805	BE123805 EST649451	968	16	2.9	339	175	DIS111	D15111 R
896	16	2.9	291	132	BB084104	BB084104 BB084104	969	16	2.9	340	15	AI032047	AI032047 OW68C04.x
897	16	2.9	292	132	BB397477	BB397477 BB397477	970	16	2.9	342	135	BB531154	BB531154
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901	16	2.9	294	167	BE484355	BE484355 170926.BA	974	16	2.9	347	120	AM837124	AM837124
902	16	2.9	295	148	BF428175	BF428175 daa05d05.	975	16	2.9	348	145	BE191530	BE191530
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906	16	2.9	296	211	AO768219	AO768219 HS-3089.B	979	16	2.9	351	110	AM066611	AM066611
907	16	2.9	298	134	BB476972	BB476972 BB476972	980	16	2.9	351	220	A2392493	A2392493
908	16	2.9	299	12	AA842835	AA842835 L30-206T3	981	16	2.9	352	117	AM573879	AM573879
909	16	2.9	300	18	AI261321	AI261321 qK24C03.x	982	16	2.9	352	139	BE775070	BE775070
910	16	2.9	300	22	AI620025	AI620025 LV47d09.x	983	16	2.9	352	139	BE775091	BE775091
911	16	2.9	301	113	AM261974	AM261974 xG29F11.x	984	16	2.9	354	110	AM078578	AM078578
912	16	2.9	301	127	BB202837	BB202837 BB202837	985	16	2.9	354	164	BE192261	BE192261
913	16	2.9	301	222	A2481257	A2481257 1M0303G24	986	16	2.9	354	221	A2442408	A2442408
914	16	2.9	302	28	AV330944	AV330944 AV330944	987	16	2.9	355	19	AI342803	AI342803
915	16	2.9	302	109	AV106832	AV106832 AV106832	988	16	2.9	356	111	AM177132	AM177132
916	16	2.9	302	226	A2704152	A2704152 RPCI-23-2	989	16	2.9	357	208	A0603963	A0603963
917	16	2.9	303	14	AA992046	AA992046 o136e10.s	990	16	2.9	359	11	AA766335	AA766335
918	16	2.9	304	122	AM993378	AM993378 RC2-BN003	991	16	2.9	360	32	AM005139	AM005139
919	16	2.9	305	32	AM029059	AM029059 wv99e01.x	992	16	2.9	360	155	R38834	R38834
920	16	2.9	305	103	AI1868211	AI1868211 t098c01.x	993	16	2.9	360	175	C61709	C61709
921	16	2.9	305	227	B260996	B260996 T8F1FE TAMU	994	16	2.9	360	175	C63503	C63503
922	16	2.9	306	6	AA366196	AA366196 EST77128	995	16	2.9	361	112	AM193056	AM193056
923	16	2.9	307	156	R93581	R93581 yq34g09.r1	996	16	2.9	362	1	AA029964	AA029964
924	16	2.9	310	119	AM740066	AM740066 BR110086	997	16	2.9	362	202	AA098350	AA098350
925	16	2.9	310	167	BE507014	BE507014 dB89902.Y	998	16	2.9	362	4	AA244309	AA244309
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947	16	2.9	325	17	AI183896	AI183896 qe23d05.x							
948	16	2.9	325	135	BB506468	BB506468 BB506468							
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957	16	2.9	330	212	AO822614	AO822614 HS-5558.A							
958	16	2.9	331	5	AA329711	AA329711 EST33382							
959	16	2.9	331	19	AI350445	AI350445 q117f10.x							
960	16	2.9	331	125	BB095729	BB095729 BB095729							
961	16	2.9	332	156	T29482	T29482 EST81442.Hu							
962	16	2.9	333	128	BB233433	BB233433 BB233433							
963	16	2.9	334	16	AI142656	AI142656 OK37h12.s							
964	16	2.9	334	109	AV090266	AV090266 AV090266							
965	16	2.9	334	157	TA1518	TA1518 EST087.Soyb							
966	16	2.9	336	19	AT354634	AT354634 qu95h11.x							
967	16	2.9	338	202	AO091312	AO091312 HS-3019.B							

## ALIGNMENTS

RESULT	1	EST
BF071768	17-OCT-2000	
db57a08.x1	Blackshear/Soares normalized Xenopus egg library	Xenopus
laevis cDNA clone IMAGE:3302582.3	' similar to TR:090Q10 Q90Q10	
DIMERIC DIHYDROD1OL DEHYDROGENASE ;	RNA sequence.	
BF071768		
BF071768.1	GI:10848383	
EST.		
African clawed frog.		
Xenopus laevis		
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;		
Xenopodinae; Xenopus.		
1 (bases 1 to 671)		
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,		
Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person		
,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,		
Waterson,R. and Wilson,R.		
Washu Xenopus EST project, 1999		
Unpublished (1999)		
Contact: Sandy Clifton, Ph.D.		
Washu Xenopus EST project, 1999		
Washington University School of Medicine		
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA		
Tel: 314 286 1800		
Fax: 314 286 1810		
Email: est@wustl.edu		
Library constructed by Bento Soares and M. Fatima Bonaldo		
(University of Iowa). DNA Sequencing by: Washington University		
Genome Sequencing Center		
Clone distribution: Xenopus clones from this library are available		
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov		
Seq. primer: -40UP from Gibco		
High quality sequence stop: 451.		

```
FEATURES
Source
Location/Qualifiers
1. 671
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:3302582"
/clone_lib="Blackshear/Soares normalized Xenopus egg
library"
/sex="female"
/tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"
/note="Vector: pT7T3-Pac; Site_1: EcoRI; Site_2: NotI;
PolyA-selected mRNA was prepared from unfertilized Xenopus
laevis eggs. The library was constructed in the vector
pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and
Soares, M.B. 'Normalization and subtraction: two
approaches to facilitate gene discovery', Genome Research
6:791-806, 1996. The first strand synthesis used a
NotI-dT18 primer; double stranded cDNAs were ligated to
EcoRI adapters, digested with NotI, and directionally
cloned into the NotI and EcoRI-digested pT7T3-Pac vector.
The library contained approximately 7.2 x 10^5
recombinants, with average insert sizes of 1-1.5 kb."

BASE COUNT      167 a      149 c      141 g      214 t
ORIGIN

Query Match      3.8%; Score 21; DB 143; Length 671;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 53 TTTCTTTCCATTACATGA 73
|||||
Db 327 TTTCTTTCCATTACATGA 347

RESULT 2
LOCUS      AQ210775      745 bp      DNA      GSS      18-SEP-1998
DEFINITION HS_2229_A1.G04_MK_CIT Approved Human Genomic Sperm Library D Homo
ACCESSION  AQ210775
VERSION     AQ210775.1 GI:3619744
KEYWORDS    GSS.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 745)
Mahaitas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
JOURNAL
MEDLINE
COMMENT     Contact: Mahaitas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2229 row: M column: 7
Class: BAC ends
High quality sequence stop: 745.
Location/Qualifiers
1. 745
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-2229 Col-7 Row-M"

FEATURES
Source
Location/Qualifiers

BASE COUNT      75 a      38 c      33 g      79 t
ORIGIN

Query Match      3.6%; Score 20; DB 162; Length 225;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 35 TAAATTTATTTCTCAGCTTT 55
|||||
Db 136 TAAATTTATTTCTCAGCTTT 156

RESULT 3
LOCUS      BE072277      225 bp      mRNA      EST      09-JUN-2000
DEFINITION QV4-BT0536-281299-060-C03 BT0536 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BE072277
VERSION     BE072277.1 GI:8418134
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 225)
Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Britones,M.R.,
Nagal,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL
MEDLINE
COMMENT     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6tz-QV4-BT0536-281
299-060-C03&ts=1999-12-28&tl=1)
Seq primer: puc 18 forward
High quality sequence stop: 225.
Location/Qualifiers
1. 225
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BR0536"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent Application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT      75 a      38 c      33 g      79 t
ORIGIN

Query Match      3.6%; Score 20; DB 162; Length 225;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 143 CTGTTAAAGCAGCTTGCT 162  
 DB 32 CTGTTAAAGCAGCTTGCT 51

RESULT 4  
 BF906208 404 bp MRNA EST 18-JAN-2001  
 LOCUS IL3-MT0267-291200-426-G10 MT0267 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION BF906208  
 VERSION BF906208.1 GI:12297667  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 404)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,  
 Nagai, M. A., da Silva, M. Jr., Zago, M. A., Bordin, S., Costa, F. F.,  
 Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,  
 Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare,  
 M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and  
 Simpson, A. J. U.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 JOURNAL 20202663  
 MEDLINE  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?IL3=IL3&IL2=IL3-MT0267-291200-426-G10&IL3=2000-12-29&IL4=1>)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 276.

FEATURES  
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 Location/Qualifiers  
 1..404  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="MT0267"  
 /dev\_stage="Adult"  
 /note="Organ: marrow; Vector: puc18; Site\_1: Sma1; Site\_2:  
 Sma1; A mini-library was made by cloning products derived  
 from ORESTES PCR (U.S. Letters Patent application No. 196  
 716 - Ludwig Institute for Cancer Research) profiles  
 into the puc 18 vector. Reverse transcription of tissue  
 mRNA and cDNA amplification were performed under low  
 stringency conditions."  
 BASE COUNT 99 a 118 c 88 g 99 t  
 ORIGIN

Query Match 3.6%; Score 20; DB 170; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 5.3;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GCCTTCTTCCCATTAACA 69  
 DB 26 GCCTTCTTCCCATTAACA 7

RESULT 5  
 AZ502214 667 bp DNA GSS 05-OCT-2000  
 LOCUS AZ502214/c  
 DEFINITION ILM0341J01R Mouse 10kb plasmid UGCCIM library Mus musculus genomic  
 clone UGCCIM0341J01 R, DNA sequence.

ACCESSION AZ502214  
 VERSION AZ502214.1 GI:10683626  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 667)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.  
 and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 JOURNAL  
 COMMENT University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0341 row: J column: 01  
 Seq primer: CACACAGCAACACGATGACC  
 Class: plasmid ends  
 High quality sequence stop: 667.

FEATURES  
 source  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCCIM0341J01"  
 /clone\_lib="Mouse 10kb plasmid UGCCIM library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: pMD42ny; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g11473211419b1AF129072.1), a copy-number  
 inducible derivative of plasmid RL. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."  
 BASE COUNT 175 a 155 c 122 g 214 t 1 others  
 ORIGIN

Query Match 3.6%; Score 20; DB 223; Length 667;  
 Best Local Similarity 100.0%; Pred. No. 5.4;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 GGATATGATTAATTTATTC 46  
 DB 612 GGATATGATTAATTTATTC 593

RESULT 6  
 AO854708 688 bp DNA GSS 12-MAY-2000  
 LOCUS AO854708  
 DEFINITION CP62172A CPTOMAGDNA1 Cryptosporidium parvum genomic, DNA sequence.

ACCESSION A0854708  
 VERSION A0854708.1 GI:6205165  
 KEYWORDS GSS.  
 SOURCE Cryptosporidium parvum.  
 ORGANISM Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Cryptosporididae; Cryptosporidium.  
 REFERENCE 1 (bases 1 to 688)  
 TITLE Strong, W.B. and Nelson, R.G.  
 JOURNAL Preliminary profile of the Cryptosporidium parvum genome: an expressed sequence tag and genome survey sequence analysis  
 MEDLINE Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)  
 COMMENT 20183851  
 CONTACT: Nelson, R. G.  
 Depts. of Medicine & Pharmaceutical Chemistry  
 San Francisco General Hospital-University of California, San Francisco  
 Box 0811, San Francisco, CA 94143-0811, USA  
 Tel: 415 206 8846  
 Fax: 415 206 3353  
 Email: malarial@lisa.ucsf.edu  
 For Annotation Data see <http://medsfh.ucsf.edu/ld/CpTags/home.html>  
 Seq primer: M13(-21) forward  
 Class: Shotgun.

FEATURES  
 source  
 1..688  
 /organism="Cryptosporidium parvum"  
 /strain="IOWA"  
 /db\_xref="taxon:5807"  
 /clone\_lib="CpIOWAGDNA1"  
 /lab\_host="E. coli XL2 Blue MRF"  
 /note="Vector: pBluescript II (SK-); Site: EcoRV; C. parvum (IOWA isolate) genomic DNA was hydrodynamically sheared to produce fragments having a light size distribution between 2-4 kb by Dr. Yvonne Thorsen of the Stanford DNA Sequencing and Technology Center (<http://sequence-www.stanford.edu/group/techdev/shear.htm>). The randomly sheared gDNA was chromatographed on Sephacryl S-400 to remove any small fragments and DNA eluting in the void volume was subcloned into an EcoRV-digested, alkaline phosphatase-treated pBluescript II (SK-) vector and transformed into E. coli strain XL2 Blue MRF. Recombinant clones from the first plating of the library were selected for sequence analysis using T3 and T7 primers."

BASE COUNT 238 a 106 c 113 g 231 t

ORIGIN

Query Match 3.6%; Score 20; DB 212; Length 688;  
 Best Local Similarity 100.0%; Pred. No. 5.4;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 518 ATATAGACAGTATTTTAAA 537  
 ||||||||||||||||||||  
 Db 274 ATATAGACAGTATTTTAAA 293

RESULT 7  
 CNS01VPE/c  
 LOCUS  
 DEFINITION  
 CNS01VPE 771 bp DNA GSS 12-MAY-2000  
 Tetraodon nigroviridis genome survey sequence T7 end of clone 199G15 of library G from Tetraodon nigroviridis, genomic survey sequence.  
 AL169403  
 AL169403.1 GI:7807460  
 GSS: genome survey sequence.  
 Tetraodon nigroviridis.  
 Tetraodon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha; Holacanthopterygii; Acanthopterygii; Percomorpha;

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source  
 1..771  
 /organism="Tetraodon nigroviridis"  
 /db\_xref="taxon:99883"  
 /clone\_lib="199G15"  
 /clone\_lib="G"  
 /note="Genoscope sequence ID : COAG199A0808UP1-end : T7"  
 Location/Qualifiers

BASE COUNT 168 a 194 c 193 g 211 t 5 others

ORIGIN

Query Match 3.6%; Score 20; DB 230; Length 771;  
 Best Local Similarity 100.0%; Pred. No. 5.5;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 TAGAGTTAAGAGCTTTAA 259  
 ||||||||||||||||||||  
 Db 97 TAGAGTTAAGAGCTTTAA 78

RESULT 8  
 CNS03B2I/c  
 LOCUS  
 DEFINITION  
 CNS03B2I 983 bp DNA GSS 15-MAY-2000  
 Tetraodon nigroviridis genome survey sequence T7 end of clone 013G02 of library G from Tetraodon nigroviridis, genomic survey sequence.  
 AL237159  
 AL237159.1 GI:7896294  
 GSS: genome survey sequence.  
 Tetraodon nigroviridis.  
 Tetraodon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Holacanthopterygii; Acanthopterygii; Percomorpha; Eucanthomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.  
 1 (bases 1 to 983)  
 Roest-Crolius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.  
 Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
 Unpublished  
 2 (bases 1 to 983)  
 Roest-Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.  
 Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence  
 Unpublished

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL

REFERENCE 3 (bases 1 to 983)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases  
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.  
FEATURES  
source  
1..983  
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/db\_xref="taxon:99883"  
/clone="013602"  
/clone\_lib="G"  
/note="Genoscope sequence ID : COBG013BD01LPI-end : T7"  
BASE COUNT 246 a 251 c 235 g 248 t 3 others  
ORIGIN  
Query Match 3.6%; Score 20; DB 230; Length 983;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 106 AATATATGGAATATGCAATT 125  
|||||  
Db 161 AATATATGGAATATGCAATT 142  
RESULT 9  
CNS0421Y 1016 bp DNA GSS 18-MAY-2000  
LOCUS Tetraodon nigroviridis genome survey sequence PUC-Orl end of clone  
DEFINITION 075F19 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
ACCESSION AL270943  
VERSION GI:7992890  
KEYWORDS GSS: genome survey sequence.  
SOURCE Tetraodon nigroviridis.  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;  
Holacanthopterygii; Acanthopterygii; Percomorpha;  
Tetraodontiformes; Tetraodontidae; Tetraodon.  
REFERENCE 1 (bases 1 to 1016)  
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bonneau,L., Billault,A., Queller,F., Saurin,W., Bernot,A. and  
Weissenbach,J.  
TITLE Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1016)  
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bernet,A., Fizames,C., Wincker,P., Brotier,P., Queller,F.,  
Saurin,W. and Weissenbach,J.  
TITLE Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 1016)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases  
COMMENT This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/Tetraodon>.  
FEATURES  
source  
1..1016  
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/db\_xref="taxon:99883"  
/clone="075F19"  
/clone\_lib="G"  
/note="Genoscope sequence ID : COBG075SC10SP1-end :

BASE COUNT 261 a 238 c 264 g 244 t 9 others  
ORIGIN  
Query Match 3.6%; Score 20; DB 231; Length 1016;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 106 AATATATGGAATATGCAATT 125  
|||||  
Db 761 AATATATGGAATATGCAATT 780  
RESULT 10  
CNS03009 1019 bp DNA GSS 17-MAY-2000  
LOCUS Tetraodon nigroviridis genome survey sequence PUC-Orl end of clone  
DEFINITION 043M02 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
ACCESSION AL253602  
VERSION GI:7974614  
KEYWORDS GSS: genome survey sequence.  
SOURCE Tetraodon nigroviridis.  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;  
Holacanthopterygii; Acanthopterygii; Percomorpha;  
Tetraodontiformes; Tetraodontidae; Tetraodon.  
REFERENCE 1 (bases 1 to 1019)  
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bonneau,L., Billault,A., Queller,F., Saurin,W., Bernot,A. and  
Weissenbach,J.  
TITLE Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1019)  
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bernet,A., Fizames,C., Wincker,P., Brotier,P., Queller,F.,  
Saurin,W. and Weissenbach,J.  
TITLE Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 1019)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases  
COMMENT This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/Tetraodon>.  
FEATURES  
source  
1..1019  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone="043M02"  
/clone\_lib="G"  
/note="Genoscope sequence ID : COBG043BG01SP1-end :  
PUC-Orl"  
BASE COUNT 221 a 265 c 250 g 276 t 7 others  
ORIGIN  
Query Match 3.6%; Score 20; DB 231; Length 1019;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 106 AATATATGGAATATGCAATT 125  
|||||  
Db 36 AATATATGGAATATGCAATT 17



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Db      252 ATGCTTGATACATTCT 234

RESULT  13
LOCUS   X61840
DEFINITION M8TSG129X Lambda uni-ZAP II Mus musculus cDNA clone Tsg129x, mRNA
sequence.
ACCESSION X61840
VERSION   X61840.1 GI:54948
KEYWORDS EST.
SOURCE    house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 288)
AUTHORS  Hoog, C.
TITLE     Isolation of a large number of novel mammalian genes by a
          differential cDNA library screening strategy
JOURNAL   Nucleic Acids Res. 19, 6123-6127 (1991)
MEDLINE   92066457
COMMENT   Contact: C. Hoog
          Dept. of Molecular Genetics
          Karolinska Institutet
          Box 60400, 10401 Stockholm, SWEDEN.
          Location/Qualifiers
            1..288
              /organism="Mus musculus"
              /strain="BALB/c"
              /db_xref="taxon:10090"
              /clone="Tsg129x"
              /clone_1lb="Lambda uni-ZAP II"
              /note="Vector: Lambda uni-ZAP II; Testis tissue.
              Differential cDNA screening strategy used."

FEATURES
  source
    1..288
      /organism="Mus musculus"
      /strain="BALB/c"
      /db_xref="taxon:10090"
      /clone="Tsg129x"
      /clone_1lb="Lambda uni-ZAP II"
      /note="Vector: Lambda uni-ZAP II; Testis tissue.
      Differential cDNA screening strategy used."

BASE COUNT      86 a      49 c      73 g      80 t
ORIGIN
Query Match      3.4%; Score 19; DB 159; Length 288;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      311 ATGCTTGATACATTCT 329
          |||||||
Db      72 ATGCTTGATACATTCT 90

RESULT  14
LOCUS   BB266564/c
DEFINITION BB266564 RIKEN full-length enriched, 10 days neonate cortex Mus
musculus cDNA A830026E08 3', mRNA sequence.
ACCESSION BB266564
VERSION   BB266564.1 GI:8963026
KEYWORDS EST.
SOURCE    house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 291)
AUTHORS  Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci,
          P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
          Hitozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
          Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
          Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
          Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
          Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata,
          Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
          Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya,
          T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,
          Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino,
          M., Muramatsu, M. and Hayashizaki, Y.
          RIKEN Mouse ESTs (Kono, H., et al.)

```

```

JOURNAL   Unpublished (2000)
COMMENT    Contact: Yoshinhide Hayashizaki
          Genome Exploration Research Group, Life Science Tsukuba Center,
          Genome Science Laboratory
          The Institute of Physical and Chemical Research (RIKEN), Genomic
          Sciences Center
          3-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
          Tel: +81-298-36-9013
          Fax: +81-298-36-9098
          Email: genome-res@rtc.riken.go.jp,
          URL: http://genome.rtc.riken.go.jp/
          Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
          N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
          Thermostabilization and thermoactivation of thermolabile enzymes by
          trehalose and its application for the synthesis of full length
          cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
          Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
          Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
          Y. and Hayashizaki, Y.
          Automated filtration-based high-throughput plasmid preparation
          system. Genome Res. 9 (5), 463-470 (1999)
          Carninci, P. and Hayashizaki, Y.
          High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
          19-44 (1999)
          Please visit our web site (http://genome.rtc.riken.go.jp) for
          further details.

FEATURES
  source
    1..291
      /organism="Mus musculus"
      /db_xref="taxon:10090"
      /clone="A830026E08"
      /clone_1lb="RIKEN full-length enriched, 10 days neonate
      cortex"
      /tissue_type="cortex"
      /dev_stage="10 days neonate"
      /lab_host="DH10B"
      /note="Site_1: SalI; Site_2: BamHI; cDNA library was
      prepared and sequenced in Mouse Genome Encyclopedia
      Project of Genome Exploration Research Group in Riken
      Genomic Sciences Center and Genome Science Laboratory in
      RIKEN. Division of Experimental Animal Research in Riken
      contributed to prepare mouse tissues. 1st strand cDNA was
      primed with a primer [5'
      GAGAGAGAGAGATCCAGACTCTTTTCTTTTCTTTTCTTTVN 3']. cDNA was
      prepared by using trehalose thermo-activated reverse
      transcriptase and subsequently enriched for full-length by
      cap-trapper. cDNA went through one round of normalization
      to Rot = 20.0 and subtraction to Rot = 459.0. Second
      strand cDNA was prepared with the primer adapter of
      sequence [5' GAGAGAGAGATCTCGAGTTAATTAATTAATTCCTCCCCCCCC
      3']. cDNA was cleaved with XhoI and BamHI. Vector: a
      modified pInscript KS(+) after bulk excision from Lambda
      FLC I."

BASE COUNT      79 a      60 c      53 g      99 t
ORIGIN
Query Match      3.4%; Score 19; DB 129; Length 291;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      138 ACATGCTGTTAAACAGT 156
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Db      274 ACATGCTGTTAAACAGT 256

RESULT  15
LOCUS   BF460484/c
DEFINITION BF460484 302 bp mRNA
          UT-M-CG0p-bmd-b-06-0-UI s1 NIH_BMAP_Ret1_S2 Mus musculus cDNA clone
          UT-M-CG0p-bmd-b-06-0-UI 3', mRNA sequence.
ACCESSION BF460484
VERSION   BF460484.1 GI:11529641

```

## KEYWORDS

EST,  
house mouse,  
Mus musculus

## SOURCE

Mus musculus

## ORGANISM

Mus musculus

## REFERENCE

Mammalia: Eutheria: Rodentia: Sclurognathi: Muridae: Murinae; Mus.  
1 (bases 1 to 302)

## AUTHORS

Bonafide, M.F., Lennon, G. and Soares, M.B.

## TITLE

Normalization and subtraction: two approaches to facilitate gene  
discovery

## JOURNAL

Genome Res. 6 (9), 791-806 (1996)

## MEDLINE

97044477

## COMMENT

Contact: Chin, H

National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mstemail.nih.gov

The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. The sequence tag present in the cDNA between the NotI site  
and the oligo-dT track served to identify it as a clone from the  
retina tissue cDNA library preparation. M.B. Soares Lab Clone  
distribution: Researchers may obtain BMAP cDNA clones from RESEARCH  
GENETICS. It should be noted that Bento Soares is generating a  
small number of additional specialized non-redundant arrays of BMAP  
cDNAs whose availability will be considered under appropriate and  
limited collaborative arrangements. The following repetitive  
elements were found in this cDNA sequence: 1-21,  
>AT\_richlow\_complexity  
Seq primer: M13 Forward  
POLYA=yes.

## FEATURES

## source

## Location/Qualifiers

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="01-M-CGOp-bmd-D-06-0-01"  
/clone\_1lb="NIH\_BMAP\_Ret4\_S2"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker. Site\_1: Not I; Site\_2: Eco RI; The  
NIH\_BMAP\_Ret4\_S2 library is a subtracted library,  
ultimately derived from mouse retina tissue libraries at  
various stages of development. For a detailed description  
of the library from which this clone was derived, please  
visit our web site at brainest.eng.uiowa.edu.  
TAG\_LIB=NIH\_BMAP\_Ret4\_S2  
TAG\_TISSUE=adult-retina  
TAG\_SEQ=GTGAGCGCGCAC"

## BASE COUNT

86 a 83 c 51 g 82 t

## ORIGIN

## Query Match

3.4%; Score 19; DB 148; Length 302;

## Best Local Similarity

100.0%; Pred. No. 18;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 ATGGTGGATACATTTCCT 329

Db 266 ATGCTTGATACATTTCCT 248

Search completed: May 31, 2001, 01:25:10  
Job time: 5437 sec.